

GenCore version 5.1.3  
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## OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 07:42:36 ; Search time 3214 Seconds

(without alignments)  
10458.538 Million cell updates/sec

Title: US-09-786-926-2

Perfect score: 1155  
Sequence: 1 atgaagcgcacgggggaaccc.....ccagcgctgcgagcatctga 1155Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.sts:\*  
11: gb.sts:\*  
12: gb.sts:\*  
13: gb.un:\*  
14: gb.vl:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
27: em.sts:\*  
28: em.un:\*  
29: em.vl:\*  
30: em.htg.hum:\*  
31: em.htg.in:\*  
32: em.htg.inv:\*  
33: em.htg.mus:\*  
34: em.htg.pin:\*  
35: em.htg.rod:\*  
36: em.htg.mam:\*  
37: em.htg.vrt:\*  
38: em.sy:\*  
39: em.htgo.hum:\*  
40: em.htgo.mus:\*  
41: em.htgo.other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1155	100.0	1566	9	HSEPD4	AJ000479 Homo sapi
2	1155	100.0	1582	9	BC014970	BC014970 Homo sapi
3	1155	100.0	41174	9	AC011547	AC011547 Homo sapi
4	1105	95.7	203481	30	AC023470	AC023470 Homo sapi
5	1104.8	95.7	1649	6	AR071762	AR071762 Sequence
6	768.8	66.6	1660	10	MM06074	MM06074 Mus muscu
7	765.6	66.3	7088	10	MM0489247	MM0489247 Mus muscu
8	756.8	65.5	278652	2	AC073809	AC073809 Mus muscu
9	752.8	65.2	172489	2	AC128579	AC128579 Rattus no
10	664.4	57.5	52806	2	AC090158	AC090158 Homo sapi
11	278.2	24.1	978	9	AY011720	AY011720 Lemur cat
12	256.8	22.2	7664	9	HSM803501	AL832194 Homo sapi
13	256	22.2	1134	9	AF022139	AF022139 Homo sapi
14	256	22.2	1137	6	AX085542	AX085542 Sequence
15	256	22.2	2327	9	HSEPD3	X83864 H. sapiens E
16	256	22.2	173341	2	AL772202	AL772202 Homo sapi
17	254.4	22.0	1137	6	AR112475	AR112475 Sequence
18	253.2	21.9	977	4	AY011726	AY011726 Artibeus
19	250.4	21.7	1197	6	AX147832	AX147832 Sequence
20	250.4	21.7	1197	6	AX286722	AX286722 Sequence
21	250.4	21.7	1197	6	AX360904	AX360904 Sequence
22	250.4	21.7	1197	6	AX376585	AX376585 Sequence
23	250.4	21.7	1197	9	AB083602	AB083602 Homo sapi
24	250.4	21.7	1197	9	AF317676	AF317676 Homo sapi
25	250.4	21.7	1198	6	AX138796	AX138796 Sequence
26	250.4	21.7	1400	6	AX253448	AX253448 Sequence
27	250.4	21.7	1695	5	AF164114	AF164114 Fugu tubr
28	250.4	21.7	2147	6	AX244600	AX244600 Sequence
29	250.4	21.7	2191	9	BC034703	BC034703 Homo sapi
30	250.4	21.7	2306	9	AF331840	AF331840 Homo sapi
31	250.4	21.7	100680	9	AC011461	AC011461 Homo sapi
32	245.2	21.2	978	4	AY059700	AY059700 Tadaria
33	245.2	21.2	978	10	AY011704	AY011704 Muscardin
34	244.2	21.1	978	10	AY011714	AY011714 Myocastor
35	243.6	21.1	2757	6	AX083645	AX083645 Sequence
36	243	21.0	978	9	AY011718	AY011718 Cynocepha
37	241	20.9	978	4	AY011732	AY011732 Triaelaph
38	240.4	20.8	1143	9	AF022137	AF022137 Homo sapi
39	240.4	20.8	1146	6	AX083646	AX083646 Sequence
40	240.4	20.8	2757	9	HUMEDG	M31210 Human endot
41	239.8	20.8	978	4	AY011694	AY011694 Sorex ara
42	239.6	20.7	978	4	AY011693	AY011693 Condylura
43	239.2	20.7	52806	2	AC090158	AC090158 Homo sapi
44	238.2	20.6	978	4	AY011734	AY011734 Okapia jo
45	237.4	20.6	1149	9	AF233365	AF233365 Homo sapi

## ALIGNMENTS

RESULT 1  
HSPD4 1566 bp mRNA linear PRI 17-NOV-1998  
LOCUS Homo sapiens mRNA for putative G-protein coupled receptor, ED66.  
DEFINITION  
ACCESSION AJ000479  
VERSION AJ000479.1 GI:3805931  
KEYWORDS edg6 gene; G-protein coupled receptor.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1566)  
AUTHORS Graeler M.H.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-1997) Graeler M.H., Molekulare Tumorgenetik,

Max-Debrueck-Centrum, Robert-Rössle-Strasse 10, 13122 Berlin,  
GERMANY  
2 (bases 1 to 1566)  
AUTHORS  
Gräler, M.H., Bernhardt, G. and Lip, M.  
TITLE  
EDG6, a novel G-protein-coupled receptor related to receptors for  
bioactive lysophospholipids, is specifically expressed in lymphoid  
tissue  
JOURNAL  
Genomics 53 (2), 164-169 (1998)  
MEDLINE  
99009331  
PUBMED  
9790765  
FEATURES  
Source  
Location/Qualifiers  
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/cell\_type="dendritic cells"  
/note="In vitro differentiated from blood cells with IL-4  
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23..1177  
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/db\_xref="GI:3805932"  
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RYVGFGLCWLALALGMLPLGNMCLAFRCSSLLPLSKRYILFCLVIFAGLAT  
IMGLYGFRIYVQSGOKAPRPAARRKARLLKTVLLILAFVGLGLADVF  
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GDCIARVNAHSGASTDSLSLRPDSFGSRSLSFRRREPLSSISVRS1"

\*sig\_peptide  
BASE COUNT 211 a 536 c 523 g 296 t  
ORIGIN

Query Match 100.0%; Score 1155; DB 9; Length 1566;  
Best Local Similarity 100.0%; Pred. No. 2.4e-140;  
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGCCAGCGGAGACCCGAGTGGCCCGAGTCTGCGCAACAGCTGGCGCGG 60  
DB 23 ATGAAGCCAGCGGAGACCCGAGTGGCCCGAGTCTGCGCAACAGCTGGCGCGG 82  
QY 61 CACAGCGGCTCATTTGTTCTGACACACACACACACACACACACACACACAC 120  
DB 83 CACAGCGGCTCATTTGTTCTGACACACACACACACACACACACACACACAC 142  
QY 121 CCGAGAGATGCGGCGCTGGGCGCCCTGCGGGGCTGTGCGTGCGCCAGCTGCGTG 180  
DB 143 CCGAGAGATGCGGCGCTGGGCGCCCTGCGGGGCTGTGCGTGCGCCAGCTGCGTG 202  
QY 181 GTGCTGAGAGACATGCTGGTGTGCTGGGCGCATCACAGCAGCATCGGTGCGAGCGTGG 240  
DB 203 GTGCTGAGAGACATGCTGGTGTGCTGGGCGCATCACAGCAGCATCGGTGCGAGCGTGG 262  
QY 241 GTCTACTATTGCTGTGATACATCACTGAGTACCTGTACAGCGGCGCGCTACTG 300  
DB 263 GTCTACTATTGCTGTGATACATCACTGAGTACCTGTACAGCGGCGCGCTACTG 322  
QY 301 GCCACGTGCTGTGCGGGGCGCGACCTTCCGTCGTGGCGCGCCAGTGGTCTTA 360  
DB 323 GCCACGTGCTGTGCGGGGCGCGACCTTCCGTCGTGGCGCGCCAGTGGTCTTA 382  
QY 361 CCGGAGGCGCTGCTCTTACAGCGCCCTGCGCGCCCTCCACCTTACAGCTGCTTACAGTGA 420  
DB 383 CCGGAGGCGCTGCTCTTACAGCGCCCTGCGCGCCCTCCACCTTACAGCTGCTTACAGTGA 442  
QY 421 GGGAGGCGCTTGTTCACCATGCTGGCGCGGTGGCGGAGAGCGGGGACCAACAGACAGC 480  
DB 443 GGGAGGCGCTTGTTCACCATGCTGGCGCGGTGGCGGAGAGCGGGGACCAACAGACAGC 502

QY 481 CCGCTCTACGCGCTTCAATCGGCTCTCTGCTGGCTGCTGCGCGCGCTGCTGGGATGCTGCT 540  
DB 503 CCGCTCTACGCGCTTCAATCGGCTCTCTGCTGGCTGCTGCGCGCGCTGCTGGGATGCTGCT 562  
QY 541 TTGCTGAGCTGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 563 TTGCTGAGCTGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 622  
QY 601 TCCAGGCGCTACATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
DB 623 TCCAGGCGCTACATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 682  
QY 661 GCGCTCTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
DB 683 GCGCTCTATGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 742  
QY 721 GCGGCGCGCGCAGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
DB 743 GCGGCGCGCGCAGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 802  
QY 781 CTGCTGCTGCTGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
DB 803 CTGCTGCTGCTGAGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 862  
QY 841 TGGGCGCAGAGTACCTGCGGCGCATGAGTGAATCTGAGCCCTGCGCTCTCAACTG 900  
DB 863 TGGGCGCAGAGTACCTGCGGCGCATGAGTGAATCTGAGCCCTGCGCTCTCAACTG 922  
QY 901 GCGGCTCAACCCCATCATCTACTCTCTCCGAGCAGGAGGAGTGTGAGAGCCGCTGCTGAG 960  
DB 923 GCGGCTCAACCCCATCATCTACTCTCTCCGAGCAGGAGGAGTGTGAGAGCCGCTGCTGAG 982  
QY 961 TTCTCTGCTGCGGCTGTCTCCGCTGCGGCTGCGGCTGCGGAGTGTGAGAGCCGCTGAG 1020  
DB 983 TTCTCTGCTGCGGCTGTCTCCGCTGCGGCTGCGGCTGCGGAGTGTGAGAGCCGCTGAG 1042  
QY 1021 GCGGCTGAGGCTCACTCGGAGCTTCCACACCGACACGCTCTGTGAGGCCCAAGGACAG 1080  
DB 1043 GCGGCTGAGGCTCACTCGGAGCTTCCACACCGACACGCTCTGTGAGGCCCAAGGACAG 1102  
QY 1081 TTTCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
DB 1103 TTTCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1162  
QY 1141 GTGCGGAGCATCTGA 1155  
DB 1163 GTGCGGAGCATCTGA 1177

RESULT 2  
BC014970 1582 bp mRNA linear PRI 04-OCT-2001  
LOCUS  
DEFINITION Homo sapiens, clone MGC:23096 IMAGE:4849349, mRNA, complete cds.  
ACCESSION BC014970  
VERSION BC014970.1 GI:15929024  
KEYWORDS MGC.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.

REFERENCE  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Dr. Daniel McVicar, DMS/NCI  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@gscc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline  
Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,  
Michael Thorne, Miranda Tsai, Natasia van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/URL at: <http://image.llnl.gov>  
Series: IRAL Plate: 34 Row: a Column: 5  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 4503458.

## FEATURES

## SOURCE

Location/Qualifiers

## CDS

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26..1180  
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RYVGFICMLLALIGMLDPLGWNCCADRSCLPLVSKRTLLCLVIFAGVAT  
IMGLYAGIFRLVGGGOKAPAPARARARLLKVLMLLAFLVCMGDLGLLADVF  
GSNMAOEYRGMWMLIAVANSVNPITISFERSRVCASVIFLCGLRLGMRGP  
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BASE COUNT 223 a 540 c 523 g 296 t

## ORIGIN

Query Match 100.0%; Score 1155; DB 9; Length 1582;  
Best Local Similarity 100.0%; Pred. No. 2,4e-140;  
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAACGCCACGGGAGACCCGGGTGGCCCCGAGTCTCGCAACAGCTGGCGCGCGG 60  
26 ATGAACGCCACGGGAGACCCGGGTGGCCCCGAGTCTCGCAACAGCTGGCGCGCGG 85  
61 CACAGCGGCTCATGTTCTGACATACACACCTGGGCGGCTGGCGCGCGCGGCGG 120  
86 CACAGCGGCTCATGTTCTGACATACACACCTGGGCGGCTGGCGCGCGCGGCGG 145  
121 CCGGAGATGGCGGCGCTGGGCGGCGCTGGCGGCGGCTGGCGGCGGCGGCGG 180  
146 CCGGAGATGGCGGCGCTGGGCGGCGCTGGCGGCGGCTGGCGGCGGCGGCGG 205  
181 GTGCTGAGAACTTGTGCTGGCGGCGCTGGCGGCGGCTGGCGGCGGCGGCGG 240  
206 GTGCTGAGAACTTGTGCTGGCGGCGCTGGCGGCGGCTGGCGGCGGCGGCGG 265  
241 GTTCTATTGCTGTGTAACATCAGCTGAGTGAACCTCTACAGGCGCGGCTAACCG 300  
266 GTTCTATTGCTGTGTAACATCAGCTGAGTGAACCTCTACAGGCGCGGCTAACCG 325  
301 GCCAAGTGTGCTGTGGGGGCGCCACCTTCGCTGTGGCGCGCGCCAGATGTTCTTA 360  
326 GCCAAGTGTGCTGTGGGGGCGCCACCTTCGCTGTGGCGCGCGCCAGATGTTCTTA 385  
361 CGGAGAGGCTGCTTTACACCGCCCTGGCGGCTTCACCTTCAGCTTCCTCACTGA 420  
386 CGGAGAGGCTGCTTTACACCGCCCTGGCGGCTTCACCTTCAGCTTCCTCACTGA 445

421 GGGAGCGCTTTGCCACCATGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480  
446 GGGAGCGCTTTGCCACCATGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 505  
481 CCGCTTACGCTTATCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
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541 TTGCTGGCTGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
566 TTGCTGGCTGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625  
601 TCCAGCGCTTACATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
626 TCCAGCGCTTACATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 685  
661 GGCCTTATGGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
686 GGCCTTATGGGCGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745  
721 GCGGCGCGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780  
746 GCGGCGCGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 805  
781 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
806 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865  
841 TGGGCGCGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900  
866 TGGGCGCGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 925  
901 GCGCTTACCGCGCATCT 960  
926 GCGCTTACCGCGCATCT 985  
961 TTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
986 TTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1045  
1021 GCGCTTACCGCGCATCT 1080  
1046 GCGCTTACCGCGCATCT 1105  
1081 TTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
1106 TTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1165  
1141 GTGCGGAGCATCTGA 1155  
1166 GTGCGGAGCATCTGA 1180

RESULT 3  
AC011547 41174 bp DNA linear PRI 29-JUN-2000  
LOCUS Homo sapiens chromosome 19 clone L1NR-272C5, complete sequence.  
DEFINITION AC011547  
ACCESSION AC011547.4 GI:8810260  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 41174)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
2 (bases 1 to 41174)  
DOE Joint Genome Institute.  
AUTHORS  
TITLE  
JOURNAL  
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 41174)  
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-JUN-2000) DOE Joint Genome Institute, 2800 Mitchell  
 Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Jun 29, 2000 this sequence version replaced gi:7711535.  
 Draft Sequence Produced by DOE Joint Genome Institute  
 www.jgi.doe.gov  
 Finishing Completed at Stanford Human Genome Center  
 www-shgc.stanford.edu  
 Quality: Phrap Quality >=40 99.9% of Sequence;  
 Estimated Total Number of Errors is 0.2.  
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 WI-15783 G22974.  
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 Best Local Similarity 100.0%; Pred. No. 1.1e-140;  
 Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 9925 ATGAAGCCACAGGGGAGCCCGGCGTCCGAGTCTCCCAACAGCTGGGCGCGG 9984  
 Oy 61 CACAGCGGCTCATGTTGTGCACTACAACACTGCGGCGGCTGGCGCGGCGG 120  
 Db 9985 CACAGCGGCTCATGTTGTGCACTACAACACTGCGGCGGCTGGCGCGGCGG 10044  
 Oy 121 CCGGAGAGTGGCGGCGTGGGCGGCGTGGGCGGCGTGGGCGGCGGCGG 180  
 Db 10045 CCGGAGAGTGGCGGCGTGGGCGGCGTGGGCGGCGTGGGCGGCGGCGG 10104  
 Oy 181 GTGCTGGAGAACTTGTGCTGCTGGGCGGCGTGGGCGGCGTGGGCGGCGG 240  
 Db 10105 GTGCTGGAGAACTTGTGCTGCTGGGCGGCGTGGGCGGCGTGGGCGGCGG 10164  
 Oy 241 GTCTACTATTGCTGGTGAACATCACTGAGTGAAGTCACTGAGGCGGCGGCT 300  
 Db 10165 GTCTACTATTGCTGGTGAACATCACTGAGTGAAGTCACTGAGGCGGCGGCT 10224  
 Oy 301 GCCAAGCTGCTGCTGCGGCGGCGGCGTGGGCGGCGTGGGCGGCGGCGG 360  
 Db 10225 GCCAAGCTGCTGCTGCGGCGGCGGCGTGGGCGGCGTGGGCGGCGGCGG 10284  
 Oy 361 CGGAGGCGCTGCTTTCACCGCGCTGCGGCGTGGGCGGCGTGGGCGGCGG 420  
 Db 10285 CGGAGGCGCTGCTTTCACCGCGCTGCGGCGTGGGCGGCGTGGGCGGCGG 10344  
 Oy 421 GGGAGAGGCTTTGCGACATGCGGCGGCGTGGGCGGAGCGAGCGGCGGCGG 480  
 Db 10345 GGGAGAGGCTTTGCGACATGCGGCGGCGTGGGCGGAGCGAGCGGCGGCGG 10404  
 Oy 481 CGGCTAGCGCTTTCATGCGGCGTGGGCGGCGTGGGCGGCGTGGGCGGCG 540  
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 Oy 601 TCCAAGCGCTACCTCTTCTGCGGCGTGGGCGGCGTGGGCGGCGTGGGCGGCG 660  
 Db 10525 TCCAAGCGCTACCTCTTCTGCGGCGTGGGCGGCGTGGGCGGCGTGGGCGGCG 10584  
 Oy 661 GGCTCTATGGGCGCATCTTCGCGGCGTGGGCGGCGGCGGCGGCGGCGGCGG 720  
 Db 10584 GGCTCTATGGGCGCATCTTCGCGGCGTGGGCGGCGGCGGCGGCGGCGGCGGCGG 10644

Db 10585 GGCTCTATGGGCGCATCTTCGCGGCGTGGGCGGCGGCGGCGGCGGCGGCGG 10644  
 Oy 721 GCGGCGCGCGCAAGGCGCGCGCTGCTGAAGAGGCTGATGATCTGCTGGCTTC 780  
 Db 10645 GCGGCGCGCGCAAGGCGCGCGCTGCTGAAGAGGCTGATGATCTGCTGGCTTC 10704  
 Oy 781 CTGCTGCTGCGGCGCGCATCTTCGCGGCGTGGGCGGCGTGGGCGGCGTGGGCGG 840  
 Db 10705 CTGCTGCTGCGGCGCGCATCTTCGCGGCGTGGGCGGCGTGGGCGGCGTGGGCGG 10764  
 Oy 841 TGGGCGGAGAGTACCTGCGGCGGCGTGGGCGGCGTGGGCGGCGTGGGCGGCGG 900  
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 SV AC023470.2  
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 DT 10-JUL-2000 (Rel. 64, Last updated, Version 5)  
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 XX  
 OS Homo sapiens (human)  
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 RA Waterston R.H.;  
 RT "The sequence of Homo sapiens clone";  
 RL unpublished.  
 XX  
 RN [2]  
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 RT ;  
 RL Submitted (14-FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RL Genome Sequencing Center, Washington University School of Medicine, 4444  
 RL Forest Park Parkway, St. Louis, MO 63108, USA  
 XX  
 CC On Feb 23, 2000 this sequence version replaced gi:6970697.  
 CC ----- Genome Center -----  
 CC Center: Washington University Genome Sequencing Center  
 CC Center code: WUGSC

CC	Web site:	http://genome.wustl.edu/gsc/index.shtml
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CC	Center project name:	H_NH0554A07
CC	-----	Summary Statistics
CC	Sequencing vector:	M13; 100%
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CC	Chemistry:	Dye-Primer ET; 100% of reads
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CC	Assembly program:	Phrap; version 0.990319
CC	Consensus quality:	185558 bases at least Q40
CC	Consensus quality:	191981 bases at least Q30
CC	Consensus quality:	199164 bases at least Q20
CC	Insert size:	200000; agarose-fp
CC	Insert size:	200581; sum-of-contigs
CC	Quality coverage:	4.59 in Q20 bases; agarose-fp
CC	Quality coverage:	4.65 in Q20 bases; sum-of-contigs
CC	-----	
CC	* NOTE:	This is a 'working draft' sequence. It currently
CC	* consists	of 30 contigs. The true order of the pieces
CC	* is not	known and their order in this sequence record is
CC	* arbitrary.	Gaps between the contigs are represented as
CC	* runs of	N, but the exact sizes of the gaps are unknown.
CC	* This	record will be updated with the finished sequence
CC	* as	soon as it is available and the accession number will
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VERSION	U006074.1	GI:3805935	
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SOURCE	Mus musculus		
ORGANISM	Mus musculus		
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AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	Submitted (11-MAY-1998) Graeler M.H., Molekulare Tumor- und Immunogenetik, Max-Debriueck-Centrum, Robert-Roessle-Str. 10, 13122 Berlin, GERMANY		
REFERENCE	2 (bases 1 to 1660)		

Authors	Gräter, M.H., Bernhardt, G. and Lipp, M.
Title	EDG6, a novel G-protein-coupled receptor related to receptors for bioactive lysophospholipids, is specifically expressed in lymphoid tissue
Journal	Genomics 53 (2), 164-169 (1998)
Medline	99009331
Pubmed	9790765
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## FEATURES

## source

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## ORIGIN

## Query Match

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Matches 927; Conservative 0; Mismatches 222; Indels 7; Gaps 3;

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Db 185609 CGGATATCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185668

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## RESULT 9

AC128579/c

LOCUS

DEFINITION

ACCESSION

AC128579

AC128579

AC128579

AC128579

AC128579

AC128579

AC128579

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AC128579.1 GI:21909352  
HTG: HTGS\_PHASE1.  
Rattus norvegicus.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
AUTHORS

1 (bases 1 to 172489)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
Alshrocks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,  
Barbaris,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,  
Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,  
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,  
Carion,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,  
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
Davila,M.R., Davis,C., Davy-Carroll,L., Dederich,D.A.,  
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,  
Doutwaile,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,  
Einhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,  
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,  
Gabriel,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,  
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Homs,F., Howard,S., Huber,U., Huliy,S., Hume,J., Jackson,L.E.,  
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Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,  
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
L.J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Loulsged,H.,  
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,  
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Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,  
Miner,G., Miner,Z., Mitchell,T., Mohabat,K., Morgan,M., Morris,S.,  
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,  
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Rivers,M., Rojas,A., Kojubokan,I., Rolfe,M., Ruiz,S., Severy,G.,  
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Sodergren,E., Sonalka,T., Sparks,A., Stanley,H., Stone,H.,  
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Tusani,K., Vasquez,L., Vera,Y., Villalón,D., Vinson,R., Wang,O.,  
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,  
Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 172489)  
Worley,K.C.  
Direct Submission  
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

COMMENT

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GYIW  
Center clone name: CH230-72A11  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 105806 bases at least Q40  
Consensus quality: 112580 bases at least Q30  
Consensus quality: 117088 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length

(see [http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 74 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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50159: gap of unknown length

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QY	121	CCGGAGG--ATATGGGGGCTTGGGGGGCCCTGCGGGGGCTGTGGTGGCGCGCAGCTGGCGG	177		
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QY	178	GTGGTGTCTGGAGAACTTGCTGTGTGGGGGCCATCACAGGCACATGCGGTGCGGACGC	237		
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QY	238	TGGGCTCTATTGCTGCTGGTGAACATCAACGCTGAGTGAAGCTTCTACAGGGCGGGCCTTAC	297		

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Qy 298	CTGGCAACGATGCTGCTGTGCGGGGGGCCGACACTTCCTGCTGGAGCGCCGACAGTGGTTC	357
Db 137532	GTGGTCAACGATGCTGCTGTGAGAACTCGACCTTCCTAGCTGTCACTGTGTGACATGGTTTC	137473
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Qy 418	GCAGGGAGGCTTTTGGCACATGATGATCGGCGCGGTGGCCGAGAGGGGGGGCCACCAAGAC	477
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DEFINITION	Homo sapiens chromosome 11 clone RP11-397J5 map 11, LOW-PASS	
ACCESSION	AC090158	
VERSION	AC090158.2 GI:13431021	
KEYWORDS	HTG; HTGS; PHASEO.	
SOURCE	Homo sapiens.	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

2 (bases 1 to 52806)  
Unpublished  
Homo sapiens chromosome 11, clone RP11-397J5

1 (bases 1 to 52806)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research  
320 Charles Street, Cambridge, MA 02141, USA  
On Mar 22, 2001 this sequence version replaced g1:12957787.  
All repeats were identified using RepeatMasker:  
Smt, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WtBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L1814  
Center clone name: 397\_J\_5

NOTE: This record contains 66 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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ACCESSION	AX085542			
VERSION	AX085542.1 GI:13275575			
KEYWORDS				
SOURCE	human. Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1137) Erickson,J., Goddard,J.G., Klefer,M. and Picker,D. Compounds which modulate the activity of an lpa receptor Patent: WO 0112838-A 5 22-FEB-2001;			
JOURNAL	Aitairgn Technologies, Inc. (US)			
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ORIGIN				
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Matches 513; Conservative	0; Mismatches 385; Indels 6; Gaps 2;			
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Dd		360 GGCCCTTTGGGGGGTCCACCTGACGCTTACTGGCCATTCGCATGAGCGGCACTTGACAAT	419	
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QY	741	CCGCGCTGCTGAAGAGCGGTGCTGATGATGCTGCTGCTCTGCTGCTGCTGGGCGCACT	800
Db	717	GGCACCTGCTGGCGGACCGGTGTGATGTGTGTAGCGCTGTTCATCGGCTCTGTGCCCACT	776
QY	801	CTTGCGGCTGCTGCTGCGCCGACGTCCTTTGGCTCCAACTCTGGGGCCAGAGATCACTCGG	860
Db	777	CTTCAATCCTCTTCTCATTTGATG---TG6CCGCGAGGGTGCAGAGGCGTCCCATCTCTT	833
QY	861	GGGCGATGAGCATGATCTCGGCGCTCGGCGCTCTCAACTCGGCGGCAACCCCATCATCTA	920
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QY	981	CCGG 984	
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LOCUS	HSEDG3		
DEFINITION	H.sapiens EDG-3 gene.	2327 bp	DNA
ACCESSION	X83864		
VERSION	X83864.1 GI:1770395		
KEYWORDS	EDG-3 gene; G-protein coupled receptor.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Emmalyola, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.		
REFERENCE	1 (bases 1 to 2327)		
AUTHORS	Yamaguchi, F., Davenport, A.P. and Brenner, S.		
TITLE	Molecular cloning of the new human EDG G-protein coupled receptor		
REFERENCE	2 (bases 1 to 2327)		
JOURNAL	Unpublished		
AUTHORS	Yamaguchi, F.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-JAN-1995) F. Yamaguchi, Molecular Genetics,		
REFERENCE	University of Cambridge, Dept. of Med., Level 5, Addenbrookes		
AUTHORS	Hospital, Hills Road, Cambridge CB2 2QQ, UK		
TITLE	Location/Qualifiers		
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BASE COUNT 445 a 702 c 587 g 593 t  
ORIGIN

Query Match 22.2%: Score 256; DB 9; Length 2327;  
Best Local Similarity 56.7%: Pred. No. 2, 9e-24;  
Matches 513; Conservative 0; Mismatches 385; Indels 6; Gaps 2;

QY 81 GCACCTACAAACACTCGGGCGGCTGGCGCGGGGCGCGGAGAGATGGCGGCTGGG 140  
DB 1183 GCATTAACAGTACGTGGGGAATGGCGGAGAGGCTGAAGGAGGCTCCGAGGCGACAC 1242  
QY 141 GGCCCTGGCGGGGCTGTGGTGGCCCAAGTGGCTGTGGTGGAGAACTGTGGT 200  
DB 1243 GCTACACACCGTGTCTTGTGTATCTGCACCTTCATCTTGGAGAACCTGATGGT 1302  
QY 201 GCTGGCGGCAATCACCAGCCATGCGGCTCGGAGCGCTGCTACTATTTGCTGGTAA 260  
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QY 261 CATCAGCTGAGTACCTGTCAAGGCGCGGCTACCTGGCCAAAGTGTCTGTGGG 320  
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QY 321 GGCGCGACCTTCCGTGTGGCGCGCCCAAGTGTCTTACGGAGAGGCTGTCTTAC 380  
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QY 621 CTGCTGTGTGATCTTTCGCGGCGTCTTGGCCACATCATGTGGGCTTATGGGCAATCTT 680  
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QY 981 CCGG 984  
DB 2077 CAGG 2080

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Job time : 3748 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 05:46:18 ; Search time 319 Seconds

(without alignments)  
8153.787 Million cell updates/sec

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Perfect score: 1155

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1155	100.0	1155	21	AAx82789 Human edg6 DNA. H
2	1155	100.0	1155	24	AB145809 Human endothelial
3	1155	100.0	1566	24	AB159511 Human endothelial
4	1155	100.0	1568	22	AA998657 Human EST-derived
5	1155	100.0	1877	21	AA299797 cDNA encoding a G-
6	1155	100.0	2270	20	AA593366 Human EDG-7 recept
7	1155	100.0	9163	24	AB145808 Human endothelial
8	1151.8	99.7	1176	20	AA593367 Human EDG-7 recept
9	1139	98.6	1637	20	AA69761 EDG-1-like G-prote

10	1104.8	95.7	1649	19	AAV68602	Nucleotide sequenc
11	894.2	77.4	4621	23	ABA05827	Human Lysoc-1 recep
12	768.8	66.6	1161	21	AAx82790	Murine edg6 DNA.
13	437.8	37.9	1343	20	AAx59377	Rat EDG-7 receptor
14	256	22.2	1137	20	AAx36567	Human EDG-3 coding
15	256	22.2	1137	22	AA500258	LPA receptor-relat
16	256	22.2	1137	24	ABL59508	Human endothelial
17	254.4	22.0	1137	21	AA222300	Human EDG3sh polyP
18	250.4	21.7	1194	22	AA165825	Nucleotide sequenc
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22	250.4	21.7	1197	24	ABK12963	DNA sequence of hu
23	250.4	21.7	1197	24	AA598065	Human DNA for pote
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25	250.4	21.7	1198	22	AAE87722	Human PFI-006 enco
26	250.4	21.7	1264	24	AA169392	Human EDG-8 recept
27	250.4	21.7	1335	24	AA598124	Human DNA for pote
28	250.4	21.7	1400	22	AA514597	Human CDNA encodin
29	250.4	21.7	1503	21	AAAD01132	Human orphan G pro
30	250.4	21.7	1503	21	AAA46033	Human G protein co
31	250.4	21.7	2147	22	AA515901	DNA encoding G-pro
32	250.4	21.7	2188	22	AAK94206	Human full-length
33	250.4	21.5	1980	21	AA169391	Human EDG-8 recept
34	248.8	21.5	1980	21	AA261489	DNA encoding a 142
35	241.6	20.9	6656	24	ABK51005	Human EDG1 genomic
36	240.4	20.8	1146	22	AAE74416	Angiogenesis prote
37	240.4	20.8	1146	24	ABK51006	Angiogenesis prote
38	240.4	20.8	2757	22	AAE74415	Human endothelial
39	240.4	20.8	2757	24	AB159506	Human edg-1 gene.
40	240.4	20.6	2774	12	AAO14147	Human EDG-1c recep
41	237.4	20.6	1149	20	AAZ09756	Human EDG-1c recep
42	237.4	20.6	4063	23	ABK42204	Genomic sequence #
43	234.4	20.3	1137	22	AAE62701	Murine EDG3 cDNA.
44	234.4	20.3	1825	24	ABD32834	Endothelial differ
45	230.2	19.9	2232	18	AAV58506	CDNA encoding p1r

#### ALIGNMENTS

RESULT 1  
AAx82789 standard; DNA: 1155 BP.

AAx82789;  
29-JUN-2000 (first entry)

Human edg6 DNA.

edg6; human; G-coupled receptor; endothelial differentiation gene;  
antimicrobial; immunomodulatory; antimicrobial; antiallergic;  
cytostatic; gene therapy; inflammation; autoimmune disease; allergy;  
tumor; leukemia; lymphoma; ss.

Homo sapiens.

DE19846979-A1.

23-MAR-2000.

13-OCT-1998; 98DE-1046979.

11-SEP-1998; 98DE-1043240.

(DE198-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.

Graeler M, Bernhardt G, Lipp M;

WPI: 2000-258069/23.

P-PSDB; AAM90862.



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PN WO200206446-A2.
XX 24-JAN-2002.
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XX 17-JUL-2001; 2001WO-US22523.
XX
XX 17-JUL-2000; 2000US-218727P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Kilem SE, Koshy B;
XX
XX WPI; 2002-171804/22.
XX
XX P-PSDB; AAM48981.
XX
XX New genetic variants of endothelial differentiation, G-protein coupled
XX receptor-6 gene for studying expression, function of the gene and
XX expressing EDG6 protein for use in screening drugs to treat cancer,
XX inflammation -
XX
XX Claim 25; Fig 2; 11pp; English.
XX
XX The present invention provides the gene, protein and cDNA sequences of
XX the human endothelial differentiation, G-protein coupled receptor 6
XX (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found
XX within the sequences. The sequences can be used in the identification of
XX the haplotype of an individual, and in the treatment of cancer,
XX angiogenesis and inflammation. The present sequence is the EDG6 cDNA,
XX the gene for which is found on chromosome 19p13.3.
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Best local similarity 100.0%; Pred. No. 6.8e-185;
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DB 481 CGGCTACGCGCTTCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
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XX Human endothelial cell differentiation gene EDG6 cDNA SEQ ID NO:11.
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XX tumour; lipid associated gene; lipid metabolism; chromosome 19p13.3;
XX gene; ss.
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XX Homo sapiens.
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XX OS
XX
XX PN WO200227028-A1.
XX
XX 04-Apr-2002.
XX
XX 27-SEP-2001; 2001WO-US30366.
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XX

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PA (HYSE-) HYSBO INC.  
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX WPI: 2001-476164/51.  
 DR P-PSDB: AAM23998.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 1: Page 536-537; 1275pp; English.  
 CC  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 SO Sequence 1568 BP; 211 A; 536 C; 525 G; 296 T; 0 other;  
 Query Match 100.0%; Score 1155; DB 22; Length 1568;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-185;  
 Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGCCACGGGGAGACCCCGGTGGCCCGGAGTCTGCCAAGCTGGGGCGCGGGG 60  
 DB 23 ATGAAGCCACGGGGAGACCCCGGTGGCCCGGAGTCTGCCAAGCTGGGGCGCGGGG 82  
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 QY 1081 TTTTGGGCGCTCCCGCTGCTGCTGACCTTTGCGAGTGGGAGCCCTGTCCAGCATCTCCAGC 1140  
 DB 1103 TTTTGGGCGCTCCCGCTGCTGCTGACCTTTGCGAGTGGGAGCCCTGTCCAGCATCTCCAGC 1162  
 QY 1141 GTGCGGAGCATCTGA 1155  
 DB 1163 GTGCGGAGCATCTGA 1177

RESULT 5  
 AA299797  
 ID AA299797 standard; cDNA: 1877 BP.  
 AC AA299797;  
 XX  
 DT 12-JUL-2000 (first entry)  
 XX  
 DE cDNA encoding a G-protein coupled receptor designated 14275 receptor.  
 KW Human: G-protein coupled receptor; GPCR; EDG receptor; 14275 receptor;  
 KW signal pathway; GPCR-mediated disorder; anaemia; neutropenia;  
 KW thrombocytopenia; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH key Location/Qualifiers  
 FT CDS 284..1438  
 FT /\*tag= a  
 FT /product= "14275 receptor"  
 XX  
 PN W0200014233-A1.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 03-SEP-1999; 99WO-US20347.  
 XX  
 PR 03-SEP-1998; 98US-0146416.  
 PR 03-SEP-1999; 99US-0390039.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Glucksmann MA, Hodge MR;  
 XX  
 DR WPI: 2000-256983/22.  
 DR P-PSDB: AAY69500.  
 XX

PT New G-protein coupled receptor used in receptor assays as a target for  
 PT diagnosis and treatment of receptor-mediated disorders including  
 PT anaemia, neutropenia or thrombocytopenia or a disorder involving  
 PT inflammation -  
 XX  
 PS Claim 3; Fig 1A-B; 117pp; English.  
 CC  
 CC The present sequence encodes a human G-protein coupled receptor (GPCR)  
 CC which is related to the EDG receptor family. The protein is designated  
 CC the 14275 receptor. The 14275 receptor participates in signalling  
 CC pathways. The 14275 polypeptide and polynucleotide are used as reagents  
 CC or targets in a receptor assay for treatment and diagnosis of  
 CC GPCR-mediated disorders. The disorders include anaemia, neutropenia or  
 CC thrombocytopenia or a disorder involving inflammation.  
 XX  
 SQ Sequence 1877 BP; 312 A; 624 C; 600 G; 341 T; 0 other;

Query Match 100.0%; Score 1155; DB 21; Length 1877;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-185;  
 Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAACGCCAGCGGAGCCCGGTCGAGTCCCTGCAACAGCTGGCGCGCGGG 60  
 Db 284 ATGAACGCCAGCGGAGCCCGGTCGAGTCCCTGCAACAGCTGGCGCGCGGG 343  
 OY 61 CACAGCGGCTCATTTGCTGCACTACAAACACTCGGGCGGCTGGCGCGGGGG 120  
 Db 344 CACAGCGGCTCATTTGCTGCACTACAAACACTCGGGCGGCTGGCGCGGGGG 403  
 OY 121 CCGGAGGATGGGGGCGGCGGCTGGGGGGGCTGTGGGTGGCGGCAAGCTGGTG 180  
 Db 404 CCGGAGGATGGGGGCGGCGGCTGGGGGGGCTGTGGGTGGCGGCAAGCTGGTG 463  
 OY 181 GTGCTGAGAACTTCTGTGCTGGCGGCATCACCAGCAATCGGTGCGGAGCTGG 240  
 Db 464 GTGCTGAGAACTTCTGTGCTGGCGGCATCACCAGCAATCGGTGCGGAGCTGG 523  
 OY 241 GTCTACTATTGCTGTGTAACATCACTGAGTACTGCTTCACGGCGCGGCTTACCTG 300  
 Db 524 GTCTACTATTGCTGTGTAACATCACTGAGTACTGCTTCACGGCGCGGCTTACCTG 583  
 OY 301 GCCAAGTGTCTGTGCGGGGCGGCACTTCGTCGGGGCGGCGGCAAGGTTCTCTA 360  
 Db 584 GCCAAGTGTCTGTGCGGGGCGGCACTTCGTCGGGGCGGCGGCAAGGTTCTCTA 643  
 OY 361 CGGAGGCGTGTCTGTACCGCGCTGGCGGCTTCACCTTCAGGCTGTCTTCACTGCA 420  
 Db 644 CGGAGGCGTGTCTGTACCGCGCTGGCGGCTTCACCTTCAGGCTGTCTTCACTGCA 703  
 OY 421 GGGGAGCGCTTGGCACCATGGTGGGGGTGGCGGAGAGCGGGGCCACCAAGACAGC 480  
 Db 704 GGGGAGCGCTTGGCACCATGGTGGGGGTGGCGGAGAGCGGGGCCACCAAGACAGC 763  
 OY 481 CGCGCTACGGCTTATCGGCGTGTGCGGTGGCGGCGGCGGCTGTGGGATCTGTGCT 540  
 Db 764 CGCGCTACGGCTTATCGGCGTGTGCGGTGGCGGCGGCGGCTGTGGGATCTGTGCT 823  
 OY 541 TTGCTGGGCTGGAACCTGCTTGCGCTTTGACCGCTGCTTCACGCTTTCCTCTAC 600  
 Db 824 TTGCTGGGCTGGAACCTGCTTGCGCTTTGACCGCTGCTTCACGCTTTCCTCTAC 883  
 OY 601 TCGAAGCGCTACATCTCTGCTGTGATCTTTGCGGGGCTGCTGGCCACCATATG 660  
 Db 884 TCGAAGCGCTACATCTCTGCTGTGATCTTTGCGGGGCTGCTGGCCACCATATG 943  
 OY 661 GGCCTTATGGGGCCATTTCCGCTGGTGCAGGCGAGCGGGCGAAGGCCCGCCAGCCCA 720  
 Db 944 GGCCTTATGGGGCCATTTCCGCTGGTGCAGGCGAGCGGGCGAAGGCCCGCCAGCCCA 1003  
 OY 721 GCGGCCCGCCCAAGGCCCGCGCTGCTGAAGAGGCTGTGATGATCTGTGGCTTC 780  
 Db 1004 GCGGCCCGCCCAAGGCCCGCGCTGCTGAAGAGGCTGTGATGATCTGTGGCTTC 1063

OY 781 CTGGTGTCTGGGGCCCACTTCTGGGCTGCTGTGGCGGACGCTTTGGCTCCAACTC 840  
 Db 1064 CTGGTGTCTGGGGCCCACTTCTGGGCTGCTGTGGCGGACGCTTTGGCTCCAACTC 1123  
 OY 841 TGGGCCAGGAGTACTGCGGGGATGAGATGATCTCTGGGCCCGCGCTCAACTCG 900  
 Db 1124 TGGGCCAGGAGTACTGCGGGGATGAGATGATCTCTGGGCCCGCGCTCAACTCG 1183  
 OY 901 GCGGTCAACCCCATCATCTACTCTTCCGACGACAGGAGGTGTGCAGAGCCGTCTCAGC 960  
 Db 1184 GCGGTCAACCCCATCATCTACTCTTCCGACGACAGGAGGTGTGCAGAGCCGTCTCAGC 1243  
 OY 961 TTCTCTGCTCGGGATGCTCTCGGCTGGGATGCGAGAGGCGCGGAGCTCTGGGCCGG 1020  
 Db 1244 TTCTCTGCTCGGGATGCTCTCGGCTGGGATGCGAGAGGCGCGGAGCTCTGGGCCGG 1303  
 OY 1021 GCGGTGAGGCTCACTCCGAGCTTCCAGCACGACGACTCTGTGAGGCCCAAGGAGCAGC 1080  
 Db 1304 GCGGTGAGGCTCACTCCGAGCTTCCAGCACGACGACTCTGTGAGGCCCAAGGAGCAGC 1363  
 OY 1081 TTTGCGGCTCCCGCTGTGCTACGTTTTCGATGCGGGAGCCCTGTCCAGCATCTCCAGC 1140  
 Db 1364 TTTGCGGCTCCCGCTGTGCTACGTTTTCGATGCGGGAGCCCTGTCCAGCATCTCCAGC 1423  
 OY 1141 GTGCGAGCATCTGA 1155  
 Db 1424 GTGCGAGCATCTGA 1438

RESULT 6  
 AAX59366  
 ID AAX59366 standard; cdna; 2270 BP.  
 XX  
 AC AAX59366;  
 XX  
 DT 20-SEP-1999 (first entry)  
 DE Human EDG-7 receptor homologue cdna.  
 DE  
 XX  
 XX

EDG-7: human; HEDG-7: G protein coupled receptor; asthma;  
 adult respiratory distress syndrome; rheumatoid arthritis;  
 KW cardiac ischaemia; acute pancreatitis; septic shock; psoriasis;  
 KW acute cyclosporin nephrotoxicity; diabetic glomerulopathy;  
 KW lung damage; diagnosis; therapy; drug screening;  
 KW antiinflammatory; ss.  
 KW  
 OS Homo sapiens.

Key Location/Qualifiers  
 FT 16..1170 /tag= a  
 FT CDS /note= "the coding region is specifically claimed  
 in Claim 4(a)"  
 FT  
 FT  
 FT

WO935106-A2.  
 PD 15-JUL-1999.  
 XX  
 PF 30-DEC-1998; 98MO-CA01196.  
 XX  
 PR 30-DEC-1997; 97US-0070184.  
 XX  
 PA (ALIX ) ALLELIX BIOPHARMACEUTICALS INC.  
 XX  
 PI Gupta AK, Munroe DG, Zastawny RJ.  
 DR WPI; 1999-419322/35.  
 DR P-PSDB; AAY06411.  
 DR  
 XX  
 XX  
 PT A nucleic acid sequence encoding human EDG-7 receptor, useful for  
 PT treating disorders associated with aberrant expression  
 XX  
 XX

PS Claim 4(a); Fig 1A; 72pp; English.





FT allele /tag- i  
replace(4531,A)  
FT allele /tag- j  
replace(4574,T)  
FT allele /tag- k  
replace(4736,T)  
FT allele /tag- l  
replace(4813,T)  
FT allele /tag- m  
replace(5068,T)  
FT allele /tag- n  
replace(5103,T)  
FT allele /tag- o  
replace(5150,A)  
FT allele /tag- p  
replace(5179,A)  
FT allele /tag- q  
replace(5301,A)  
FT allele /tag- r  
replace(5333,A)  
FT allele /tag- s  
replace(5448,C)  
FT allele /tag- t  
replace(5560,A)  
FT allele /tag- u  
replace(5580,A)  
FT allele /tag- v  
replace(5587,T)  
FT allele /tag- w  
replace(5606,C)  
FT allele /tag- x  
MO200206446-A2.  
XX 24-JAN-2002.  
XX 17-JUL-2001: 2001WO-US22523.  
XX 17-JUL-2000: 2000US-218727P.  
XX (GENA-) GENAISSANCE PHARM INC.  
XX PI Klem SE, Koshy B;  
XX WPI: 2002-171804/22.  
XX P-PSDB: AAM48981.  
XX New genetic variants of endothelial differentiation, G-protein coupled  
PT receptor-6 gene for studying expression, function of the gene and  
PT expressing Edg6 protein for use in screening drugs to treat cancer,  
PT Inflammation -  
XX Claim 20: Fig 1: 111pp; English.  
XX The present invention provides the gene, protein and cDNA sequences of  
CC the human endothelial differentiation, G-protein coupled receptor 6  
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found  
CC within the sequences. The sequences can be used in the identification of  
CC the haplotype of an individual, and in the treatment of cancer,  
CC angiogenesis and inflammation. The present sequence is the Edg6 gene,  
CC which is found on chromosome 19p13.3.  
XX SQ Sequence 9163 BP; 1730 A; 2757 C; 2622 G; 2054 T; 0 other;  
Query Match 100.0%; Score 1155; DB 24; Length 9163;  
Best Local Similarity 100.0%; Pred. 6.8e-185;  
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4070 CACAGCCGCTCATTTGTTCTGCACATCAACACATCGGGCCGGCTGGCCGGGGGGG 4129  
Oy 121 CCGAGAGATGGCGGCTGGGGGCTGGGGGGCTGTGCTGGCCGACGCTGCTGGT 180  
Db 4130 CCGAGAGATGGCGGCTGGGGGCTGGGGGGCTGTGCTGGCCGACGCTGCTGGT 4189  
Oy 181 GTGCTGAGAACTTGTGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGG 240  
Db 4190 GTGCTGAGAACTTGTGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGG 4249  
Oy 241 GTTACTATTGCTGGTGAACATCAGCTGAGTACCTGCTCAGCGGGGCTTACTG 300  
Db 4250 GTTACTATTGCTGGTGAACATCAGCTGAGTACCTGCTCAGCGGGGCTTACTG 4309  
Oy 301 GCCAACCTGCTGCTGTCGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 360  
Db 4310 GCCAACCTGCTGCTGTCGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 4369  
Oy 361 CGGAGGGCTGCTGCTTTCACCGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 420  
Db 4370 CGGAGGGCTGCTGCTTTCACCGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 4429  
Oy 421 CGGAGGGCTTTCACCGATGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 480  
Db 4430 CGGAGGGCTTTCACCGATGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 4489  
Oy 481 CGGCTTACGGCTTTCACCGATGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGG 540  
Db 4490 CGGCTTACGGCTTTCACCGATGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGG 4549  
Oy 541 TTGCTGGGCTGGAACGCTGTCGGGCTTTCACCGCTGCTGACGCTTTCGCTTAC 600  
Db 4550 TTGCTGGGCTGGAACGCTGTCGGGCTTTCACCGCTGCTGACGCTTTCGCTTAC 4609  
Oy 601 TCACAGGCTTACCTCTTTCGCTGCTGGTATCTTCGCGGCTGCTGCTGCTGCTATG 660  
Db 4610 TCACAGGCTTACCTCTTTCGCTGCTGGTATCTTCGCGGCTGCTGCTGCTGCTATG 4669  
Oy 661 GGCTCTATGGGGGCTATCTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Db 4670 GGCTCTATGGGGGCTATCTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4729  
Oy 721 CGGCGCGCGCGCAAGCGCGCGCGCTGCTGAAGACGCTGCTGCTGCTGCTGCTG 780  
Db 4730 CGGCGCGCGCGCAAGCGCGCGCGCTGCTGAAGACGCTGCTGCTGCTGCTGCTG 4789  
Oy 781 CTGCTGTGCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Db 4790 CTGCTGTGCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4849  
Oy 841 TGGGCCAGAGTACTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 4850 TGGGCCAGAGTACTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4909  
Oy 901 CGGCTCAACCCATCATCTTTCGCGAGCAGAGAGTGGAGAGCGCTGCTGCTGCTG 960  
Db 4910 CGGCTCAACCCATCATCTTTCGCGAGCAGAGAGTGGAGAGCGCTGCTGCTGCTG 4969  
Oy 961 TTCTCTGCTGCGGGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1020  
Db 4970 TTCTCTGCTGCGGGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 5029  
Oy 1021 GCGCTGAGGCTCATCTCGGAGTTTCACACACGACCTGCTGAGAGCCAGGAGCAGC 1080  
Db 5030 GCGCTGAGGCTCATCTCGGAGTTTCACACACGACCTGCTGAGAGCCAGGAGCAGC 5089  
Oy 1081 TTTCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
Db 5090 TTTCGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5149  
Oy 1141 GTGCGGAGCATCTGA 1155  
|||||

Db 5150 GTGCGGAGCATCTGA 5164

## RESULT 8

ID AAX59367 standard; cDNA; 1176 BP.

AC AAX59367;

DT 20-SEP-1999 (first entry)

DE Human EDG-7 receptor homologue cDNA.

KW EDG-7, human; HEDG-7: G protein coupled receptor; asthma;  
 KW adult respiratory distress syndrome; rheumatoid arthritis;  
 KW cardiac ischaemia; acute pancreatitis; septic shock; psoriasis  
 KW acute cyclosporin nephrotoxicity; diabetic glomerulopathy;  
 KW lung damage; diagnosis; therapy; drug screening;  
 KW antiinflammatory; ss.

OS Homo sapiens.

FH	key	Location/Qualifiers
1		
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FT	CDS	13..1167
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/note= "the coding region is specifically claimed  
in claim 4(a)"

PN W09935106-A2.

PD 15-JUL-1999.

PF 30-DEC-1998; 98WO-CA01196.

PR 30-DEC-1997; 97US-0070184.

PA<sup>-</sup> (ALLX) ALLELIX BIOPHARMACEUTICALS INC.

PI Gupta AK, Munroe DG, Zastawny RL,

DR. WPI; 1999-419322/35.

XX  
XX

PT treating disorders associated with aberrant expression

PS Claim 4(b); Fig 1B; 12pp; English.

This nucleotide sequence, the coding region of which is claimed, CC codes for a novel human homologue of the Edg-7 receptor, i.e. CC HEDG-7 (see AY06411), a 7-transmembrane G protein coupled receptor. CC The sequence comprises the CDNA insert of clone p3-hedg7 M10, CC which was obtained from human Jurkat T-cell CDNA by PCR CC amplification to a hedg-7 sequence (see AX59366) obtained from BAC CC identical to (see also AX59361-72). The sequence is nearly CC identical to a hedg-7 gene was mapped to chromosome 1p13.3. CC Also claimed are an expression vector comprising a HEDG-7 nucleotide CC sequence, a host cell, the isolated and purified HEDG-7 receptor, CC and methods of using HEDG-7 receptor to identify potential HEDG-7 CC ligands and antagonists. The hedg-7 nucleotide sequence can be CC used in an assay to detect inflammation or disease associated with CC abnormal levels of HEDG-7 expression. Diagnosis of aberrant CC expression of HEDG-7 can accelerate diagnosis and proper treatment CC of abnormal conditions, e.g. adult respiratory distress, asthma, CC rheumatoid arthritis, cardiac ischemia, acute pancreatitis, septic CC shock, psoriasis, acute cyclosporin nephrotoxicity and early CC diabetic glomerulopathy, as well as lung damage following exposure CC to cigarette smoke, asbestos or silica.

Sequence 1176 BP; 145 A; 419 C; 387 G; 225 T; 0 other;

Query Match	99.7%;	Score 1151.8;	DB 20;	Length 1176;
Best Local Similarity	99.8%;	Pred. No. 2.3e-184;		

Matches 1153; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATMAAGCCACGGGAGACC	CCGCTGGCCCCCGAAGTCCTCCAAACAGCTGGCGGCGGG	60
Db	13	ATGAACGCCACGGGAGACC	CCGGTGGCCCCCGAAGTCCTCCAAACAGCTGGCGGCGGG	72
QY	61	CACAGCCGGCTCATTTGTTCTGCATCAACCACTGGGGCCGGCTGGCCGGCGGGGGG	120	
Db	73	CACAGCCGGCTCATTTGTTCTGCATCAACCACTGGGGCCGGCTGGCCGGCGGGGGG	132	
QY	121	CCGAGAGATGGGGGCTGGGGGCGCTGGGGGGGCTGGGGGGGCTGGGGGCTGGGGTGG	180	
Db	133	CCGAGAGATGGGGGCTGGGGGCGCTGGGGGGGCTGGGGGGGCTGGGGGGGCTGGGGTGG	192	
QY	181	GTGCTGAGAACTTCTGGTGTGGCGGGCCATACACAGCCCAATGGCTGGCGAGCGTGG	240	
Db	193	GTGCTGAGAACTTCTGGTGTGGCGGGCCATACACAGCCCAATGGCTGGCGAGCGTGG	252	
QY	241	GTCTACTATTGCTGGTGTGAACATCAACGCTGAATGACCTGTACAGGGGGGGGCGCTAACCTG	300	
Db	253	GTCTACTATTGCTGGTGTGAACATCAACGCTGAATGACCTGTACAGGGGGGGGCGCTAACCTG	312	
QY	301	GGCAACGTCTGCTGGCGGGGGCCGACACTTCCGTCGTGGCGCCGCGCCAGTGGTTCTGA	360	
Db	313	GGCAACGTCTGCTGGCGGGGGCCGACACTTCCGTCGTGGCGCCGCGCCAGTGGTTCTGA	372	
QY	361	CGGGAGGGGCTGCTTTCACCGGCGCTGGCGGCTCCACCTTACGCTGTCTTCACTGCA	420	
Db	373	CGGGAGGGGCTGCTTTCACCGGCGCTGGCGGCTCCACCTTACGCTGTCTTCACTGCA	432	
QY	421	GGGAGACGCTTGGCCACCAATGGTGGGGGGGGGGGGGAGAGGGGGGCAACAAAGACAGC	480	
Db	433	GGGAGACGCTTGGCCACCAATGGTGGGGGGGGGGGGGAGAGGGGGGCAACAAAGACAGC	492	
QY	481	CGGCTTACGGCTTCATCGGCGCTCTGCTGAGCTGGCCGCGCTGCTGGGGAGTGTGCTCT	540	
Db	493	CGGCTTACGGCTTCATCGGCGCTCTGCTGAGCTGGCCGCGCTGCTGGGGAGTGTGCTCT	552	
QY	541	TTGCTGGGGCTGGAATGCTGCTGTGGCGCTTTGACCGCTGTCCAGCGCTTGTGGCCCTTCAAC	600	
Db	553	TTGCTGGGGCTGGAATGCTGCTGTGGCGCTTTGACCGCTGTCCAGCGCTTGTGGCCCTTCAAC	612	
QY	601	TTCAGGGGCTACAACTCTTCTGCTGGTATCTTGGCGGGGCTCTCTGGGCAACATCATG	660	
Db	613	TTCAGGGGCTACAACTCTTCTGCTGGTATCTTGGCGGGGCTCTCTGGGCAACATCATG	672	
QY	661	GGCCTTATGSGGGCCATCTTCGCGCTGGTGCAGGGCCAGGGGCGAAGAGCCCCACGGCCCA	720	
Db	673	GGCCTTATGSGGGCCATCTTCGCGCTGGTGCAGGGCCAGGGGCGAAGAGCCCCACGGCCCA	732	
QY	721	GGGCGCGCGGCAAGGGCGCGCGCTGCTGAAGAGGGTGTGAATGATCTGCTGGGCTTC	780	
Db	733	GGGCGCGCGGCAAGGGCGCGCGCTGCTGAAGAGGGTGTGAATGATCTGCTGGGCTTC	792	
QY	781	CTGCTGTGCTGGGGCCCACTTTCGGGCTGCTGGCGCACAGCTTTTGGCTCCAACTTC	840	
Db	793	CTGCTGTGCTGGGGCCCACTTTCGGGCTGCTGGCGCACAGCTTTTGGCTCCAACTTC	852	
QY	841	TGGGCCACGAGTACCTGCGGGGCGATGAGACTGATCTGTGGCGCTGGCGCGCTGCTCAACTCG	900	
Db	853	TGGGCCACGAGTACCTGCGGGGCGATGAGACTGATCTGTGGCGCTGGCGCGCTGCTCAACTCG	912	
QY	901	GGGGTCAACCCCATCATCTACTTCTTCGCGAGCAGGAGAGTGTCAAGAGCGGTGCTCAGC	960	
Db	913	GGGGTCAACCCCATCATCTACTTCTTCGCGAGCAGGAGAGTGTCAAGAGCGGTGCTCAGC	972	
QY	961	TTTCTTCTGCTGGGGTGTCTTCGGGCTGGGCTGCGATGCGAGGGCCCGGGGACTGCTTGGCCGG	1020	
Db	973	TTTCTTCTGCTGGGGTGTCTTCGGGCTGGGCTGCGATGCGAGGGCCCGGGGACTGCTTGGCCGG	1032	
QY	1021	GCGGTGAGGCTCACTCCGGAGGCTTCCACACGACGAAAGCTTCTGAGGCGCAAGGAGCAGC	1080	
Db	1033	GCGGTGAGGCTCACTCCGGAGGCTTCCACACGACGAAAGCTTCTGAGGCGCAAGGAGCAGC	1092	



Db 890 TGGGCCAGGATGACTGCGGGGATGAGTGGATCTTGCCCTGGCCCTCTCAACTGG 949  
QY 901 GCGGTCAACCCCATCATCTACTCTTCCGACAGGAGGTGTGACAGCGCTGTACG 960  
Db 950 GCGGTCAACCCCATCATCTACTCTTCCGACAGGAGGTGTGACAGCGCTGTACG 1009  
QY 961 TTCTCTGCTGCGGGGTCTCCGGGCGGAGATGCGAGGGCGCGGAGACTGCGGCGG 1020  
Db 1010 TTCTCTGCTGCGGGGTCTCCGGGCGGAGATGCGAGGGCGCGGAGACTGCGGCGG 1069  
QY 1021 GCGGTCAACCCCATCATCTACTCTTCCGACAGGAGGTGTGACAGCGCTGTACG 1080  
Db 1070 GCGGTCAACCCCATCATCTACTCTTCCGACAGGAGGTGTGACAGCGCTGTACG 1129  
QY 1081 TTCTCTGCTGCGGGGTCTCCGGGCGGAGATGCGAGGGCGCGGAGACTGCGGCGG 1140  
Db 1130 TTCTCTGCTGCGGGGTCTCCGGGCGGAGATGCGAGGGCGCGGAGACTGCGGCGG 1189  
QY 1141 GTGGGAGCATCTGA 1155  
Db 1190 GTGGGAGCATCTGA 1204

RESULT 10

AAV68602 standard; DNA; 1649 BP.

AAV68602;

16-FEB-1999 (first entry)

Nucleotide sequence of an edg-1 receptor.

XX NEDG; edg-1-like receptor; stimulation; cell proliferation; cancer;  
KW genetic defect; sickle cell anaemia; agonist; antagonist; antibody;  
KW probe; ss.  
XX

OS Homo sapiens.

XX Key Location/Qualifiers

XX FT CDS 10..1539  
XX FT /\*tag= a  
XX FT /product= "edg-1-like receptor"  
XX FT /transl\_except= (pos: 67..69, aa: Xaa)  
XX FT /transl\_except= (pos: 85..87, aa: Xaa)  
XX FT /note= "Xaa= unknown"

XX MO9848016-A1.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-US07830.

XX 24-APR-1997; 97US-0845566.

XX (INCY-) INCYTE PHARM INC.

XX Au-Young J, Guegler KJ.

XX WPI; 1998-609989/51.

XX P-PSDB; AAM80955.

XX New Edg-1 like receptor. NEDG - useful, e.g. to stimulate cell  
XX proliferation and screen for antagonists to treat disorders of  
XX excessive cell proliferation such as cancers

XX Claim 4; Fig 1A-1E; 63pp; English.

XX This is the nucleotide sequence of an edg-1-like receptor (NEDG), used  
XX in the method of the invention. NEDG can be used to stimulate cell  
XX proliferation, especially by expressing encoding polynucleotides,  
XX either in vivo (e.g. to promote cell regeneration/differentiation) or  
XX in vitro (e.g. to stimulate cell proliferation for transplantation).

CC Such administration may be useful therapeutically, e.g. to stimulate  
CC proliferation of cells selected for their ability to fight an  
CC infection or a cancer, or correct a genetic defect, e.g. sickle cell  
CC anaemia. It can be used to screen for agonists (useful to  
CC treat/prevent disorders of abnormal cell growth and differentiation  
CC as above) and antagonists, and to generate antibodies. The antagonists  
CC can be combined with a suitable carrier in pharmaceutical compositions,  
CC useful to treat/prevent disorders of excessive cell proliferation,  
CC especially cancers. The NEDG-specific antibodies may be used directly  
CC as antagonists, or indirectly as a targeting or delivery mechanism  
CC to bring pharmaceutical agents to NEDG-expressing cells. They are  
CC also useful to diagnose conditions or diseases characterised by NEDG  
CC expression, and to monitor for therapeutic interventions. They are  
CC useful to produce antisense sequences for therapeutic administration to  
CC modulate/prevent NEDG expression. They may also be used to produce  
CC probes useful to detect related sequences, or for gene mapping.

SQ Sequence 1649 BP; 226 A; 539 C; 543 G; 318 T; 23 other;

Query Match 95.7%; Score 1104.8; DB 19; Length 1649;

Best Local Similarity 99.2%; Pred. No. 1.7e-176; Matches 1150; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

QY 1 ATGAACGCCAGCGGGGACCCCGGTGGCCCGAGTCCCTGCCAAGCTGGCGCGCGG 60  
Db 10 ATGAACGCCAGCGGGGACCCCGGTGGCCCGAGTCCCTGCCAAGCTGGCGCGCGG 69  
QY 61 CACAGCGCGCTCATTTTGTGTGCACTACACCACTCGCGCGCGCTGGCGCGCGG 120  
Db 70 CACAGCGCGCTCATTTTGTGTGCACTACACCACTCGCGCGCGCTGGCGCGCGG 129  
QY 121 CCGGAGATGCGCGCGCTGGGGGCGCTGCGGGGCTGCTGCGGCGCGCACTGCTG 180  
Db 130 CCGGAGATGCGCGCGCTGGGGGCGCTGCGGGGCTGCTGCGGCGCGCACTGCTG 189  
QY 181 GTGCTGAGAACTTGTGCTGTGCTGCGCGCGCACTACCAAGCAATGGGTGCGAGCT 240  
Db 190 GTGCTGAGAACTTGTGCTGTGCTGCGCGCGCACTACCAAGCAATGGGTGCGAGCT 249  
QY 241 GTCTACTATTGCTGCTGGAACATCACGCTGAGTACCTGCTCAAGCGCGCGCT 300  
Db 250 GTCTACTATTGCTGCTGGAACATCACGCTGAGTACCTGCTCAAGCGCGCGCT 309  
QY 301 GCCAAGCTGCTGTGCTGCGGGGCGCGCACTTCCGTGTGGCGCGCGCACTGTCT 360  
Db 310 GCCAAGCTGCTGTGCTGCGGGGCGCGCACTTCCGTGTGGCGCGCGCACTGTCT 369  
QY 361 GCGGAGGCGCTGCTGTGCAACCGCGCGCTGCGCGCGCTGCGCGCGCTGCTGCA 420  
Db 370 GCGGAGGCGCTGCTGTGCAACCGCGCGCTGCGCGCGCTGCGCGCGCTGCTGCA 429  
QY 421 GCGGAGGCGCTTGTGCAACCGCGCGCTGCGCGCGAGAGCGGGGCGCAACAGAC 480  
Db 430 GCGGAGGCGCTTGTGCAACCGCGCGCTGCGCGCGAGAGCGGGGCGCAACAGAC 489  
QY 481 CCGCTCTACGCGCTTGTGCAACCGCGCGCTGCGCGCGAGAGCGGGGCGCAACAG 540  
Db 490 CCGCTCTACGCGCTTGTGCAACCGCGCGCTGCGCGCGAGAGCGGGGCGCAACAG 549  
QY 541 TTGCTGGGCTGGAACCTGCTGCGCGCTTGTGCGCGCGAGAGCGGGGCGCAACAG 600  
Db 550 TTGCTGGGCTGGAACCTGCTGCGCGCTTGTGCGCGCGAGAGCGGGGCGCAACAG 609  
QY 601 TCAAGGCGCTCATCTTGTGCTGCTGATCTTCCCGCGCGCTGCGCGCGAGAGCG 660  
Db 610 TCAAGGCGCTCATCTTGTGCTGCTGATCTTCCCGCGCGAGAGCGGGGCGCAACAG 669  
QY 661 GCGCTCTATGCGCGCATCTTCCGCTGCTGAGCGCGCGAGAGCGGGGCGCAACAG 720  
Db 670 GCGCTCTATGCGCGCATCTTCCGCTGCTGAGCGCGCGAGAGCGGGGCGCAACAG 729  
QY 721 GCGGCGCGCGCAAGCGCGCGCTGCTGAGAGCGGGGCGAGAGCGGGGCGCAACAG 780

Db 730 GCGGCCCGCCGCAAGGCCCGCCGCTGCTGAAGAGGCTGTGATGATCTGCTGGCCTTC 789  
QY 781 CTGATGTGCTGGGGGCCCACTCTTC-GGGCTGCTGCTGGGCCGACGCTTTGGCTCCAACTT 839  
Db 790 CTGATGTGCTGGGGGCCCACTCTTCGGGGCTGCTGCTGGGCCGACGCTTTGGCTCCAACTT 849  
QY 840 CTGGGCCCAAGAGTACCTTGGGGGATGAGTACCTTGGGCCCTGGCCGCTCCAACTC 899  
Db 850 CTGGGCCCAAGAGTACCTTGGGGGATGAGTACCTTGGGCCCTGGCCGCTCCAACTC 909  
QY 900 GCGGCTCAACCCCATCATCTACTCTCTCCGACGACAGGAGGTGTCAAGAGCCGTGCTCAG 959  
Db 910 GCGGCTCAACCCCATCATCTACTCTCTCCGACGAGGAGGTGTCAAGAGCCGTGCTCAG 969  
QY 960 -CTTCTCTGCTGCGGGGTCTCCGCTGAGGATGCGAGGGGCC-GGGGACCTGCTGGCC 1017  
Db 970 CTTCTCTGCTGCGGGGTCTCTCCGGCTGGGATGCGAGGGGCCGCGGGGACTGCTGGCC 1029  
QY 1018 GCGGCGCTGAGAGCTACTCGGAGCCTTCC-ACACGCAAGCTCTCTGAGGCCCAAGGGA 1076  
Db 1030 GCGGCGCTGAGAGCTACTCGGAGCCTTCCAAACACGACAGCTCTGAGGCCCAAGGGA 1089  
QY 1077 CAGCTTTGCGGGCTCCGCTGCTGAGCTTCGAGTTCGAGTGGGAGAGCCCTGCTCAGACTTC 1136  
Db 1090 CAGCTTTGCGGGCTCCCGCTGCTGAGCTTCGAGTTCGAGTGGGAGAGCCCTGCTCAGACTTC 1149  
QY 1137 CAGCGTGGGAGCATCTGA 1155  
Db 1150 CAGCGTGGGAGCATCTGA 1168  
RESULT 11  
ABAO5827  
ID ABA05827 standard; cDNA: 4621 BP.  
AC ABA05827;  
XX  
DT 15-MAR-2002 (first entry)  
XX  
DE Human Lyso-1 receptor coding sequence.  
XX  
KW Human; Lyso-1 receptor; G-protein coupled receptor; chromosome 11p;  
KW ED66 receptor; Gessler-Wilm's tumour; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1196..2222  
FT /tag= a  
FT /product= "Lyso-1 receptor"  
XX  
PN DE10007629-A1.  
XX  
PD 23-AUG-2001.  
XX  
PF 21-FEB-2000; 2000DE-1007629.  
XX  
PR 21-FEB-2000; 2000DE-1007629.  
XX  
PA (BRUE/) BRUESS M.  
PA (BOEN/) BOENISCH H.  
XX  
PI Bruess M, Boenisch H;  
XX  
DR WPI: 2001-607848/70.  
DR P-PSDB: ABB04481.  
XX  
PT New gene encodes a polypeptide useful for diagnosing Gessler-Wilm's  
PT tumor, comprising the Lyso-1 receptor which is homologous to the ED66  
PT receptor -  
XX  
PS Disclosure; Column 4; App; German.  
XX

CC The present invention provides a human gene encoding a polypeptide  
CC comprising the Lyso-1 receptor, which is homologous to the ED66 receptor.  
CC The protein is a G-protein coupled receptor, and the gene is found on  
CC chromosome 11p. The sequences can be used to diagnose Gessler-Wilm's  
CC tumour. The present sequence is the coding sequence of the invention.  
XX  
SQ Sequence 4621 BP; 842 A; 1386 C; 1381 G; 1009 T; 3 other;  
Query Match 77.4%; Score 894.2; DB 23; Length 4621;  
Best local similarity 93.9%; Pred. No. 3, 1e-141;  
Matches 1085; Conservative 0; Mismatches 48; Indels 22; Gaps 14;  
QY 1 ATGAAACCCACAGGGGACCCCGGTTGGCCGAGTCTGCTCCAAAGCTGGCGCGCGG 60  
Db 1196 ATGAAACCCACAGTGAACCCCGGTTGGCCCGAGTCTGCTCCAAAGCTGGCGCGCGG 1255  
QY 61 CACAGCCGGCTCATTTGCTGCACTACAAACACATCGGCGCGGTTGGCGCGCGG 120  
Db 1256 CACAGCCGGCTCATTTGCTGCACTACAAACACATCGGCGCGGTTGGCGCGCGG 1314  
QY 121 CCGGAGATGGCGGCTGGGGGCTCTGCGGGGCTGTGGTGGCCGCAAGCTGCTGTG 180  
Db 1315 CCGGAGATGGAGCGCCCTGGGAGCTGGCGGGGTGTGGT-----GCCGCAAGTGTCTGTG 1369  
QY 181 GTGCTGAGAACTTGTGCTGGTGGGCGCCATCAGCAGGCCAATGGGTCGAGCGCTGG 240  
Db 1370 GTGCTGAGAACTTGTGCTGGTGGGCGCCATCAGCAGGCCAATGGGTCGAGCGCTGG 1429  
QY 241 GTCTACTATTGCTGTGTAACATACGCTGAGTGAATGACCTGCTCAAGGCGCGCTTACTG 300  
Db 1430 GTCTACTATTGCTGTGTAACATACGCTGAGTGAATGACCTGCTCAAGGCGCGCTTACTG 1487  
QY 301 GCCAAGCTGCTGTGTCGGGGGCGCCGACCTTCCGCTGTGGCGCGCCGCAAGTGTCTTA 360  
Db 1488 GGCACAGTGTGCTGTGGGGG--CCGACCTTCCGCTGTGGCGCGCCGCAAGTGTCTTA 1545  
QY 361 CCGGAGGCGCTGCTTTCACCGCCCTGGCGCGCTCCACCTTCAAGCTGTCTTCACTGA 420  
Db 1546 CCGGAGGCGCTGCTTTCACCGCCCTGGCGCGCTCCACCTTCAAGCTGTCTTCACTGA 1605  
QY 421 GGGGAGCGCTTTCACCATGTTGGGGCGGTGGCCGAGAGCGGGGCCCAAGACCAAG 480  
Db 1606 GGGCAGCGCTTTC-CACCATGTTGGGGCGGTGGAC---ACGTGCGGGGCCCAAGACCAAG 1661  
QY 481 CCGCTTACGGCTTTCATCGGCGCTGCTGCTGCTGGCGCGCGCTGGGAGTGTGCTGCT 540  
Db 1662 CCGCTTAC-GCTTTCATCGGCGCTGCTGCTGCTGGCGCGCGCTGGGAGTGTGCTGCT 1720  
QY 541 TTGCTGGGCTGGAATGCTGTGGCTTTTGAACGCTGCTCAGGCTTCTGCCCCCTTAC 600  
Db 1721 TTGCTGGGCTGGAATGCTGTGGGCTTTTGAACGCTGCTCAGGCTTCTGCCCCCTTAC 1780  
QY 601 TTCAGCGCTACATCTCTTTCGCTGGATCTTTCGCGGGCTCTGGCCACCATATG 660  
Db 1781 TTCAGCGCTACATCTCTTTCGCTGGATCTTTCGCGGGCTCTGGCCACCATATG 1840  
QY 661 GGCCTTATGGGCGCATCTTCCGCTGTGTGAGGCGCAGGCGCAGAGCCCAAGCCCAAGCCCA 720  
Db 1841 GGCCTTATGGGCGCATCTTCCGCTGTGTGAGGCGCAGGCGCAGAGCCCAAGCCCA 1899  
QY 721 GCGGCGCGCGCAGAGCGCGCGCTGCTGTAAGACGCTGTGATGATCTCTGTGGCTTC 780  
Db 1900 GCGTCC--GCCGCAAGCGCGCGCGCTGTGAAGACGCTGTGATGATCTCTGTGGCTTC 1957  
QY 781 CTGATGTGCTGGGGCCCACTCTTGGGGCTGCTGGCGCGAGCGTTCGCTCCAACTC 840  
Db 1958 CTGATGTGCTGGGGCCCACTCTTGGGGCTGCTGGCGCGAGTTCGCTCCAACTC 2017  
QY 841 TGGGCCCAAGAGTACCTGCGGGCATGAGTGAATGACTGTGGCCGCTGCTCAACTCG 900  
Db 2018 TGGGCCCAAGAGTACCTGCGGGCATGAGTGAATGACTGTGGCCGCTGCTCAACTCG 2077  
QY 901 GCGGTCAACCCCATCATCTACTCTTCCGACAGCAGGAGGTGTGACAGCCGCTCTAGC 960



Qy	1018	CGGCGCGCTGAGAGCGACATCTCGGAGCTTCACGACCGACGACTCTGTGAGAGCCACAGGAC	1077
Db	1024	CGGATACCGGAGGCCCACTCGGAGCATCCACACTGACAGCTCTCTGAGGCCACAGGAC	1083
Qy	1078	AGCTTTGCGCGGCTCCCGCTGCTGACGTTTGGAGATGCGGGAGCCCGTGTACACATCTCC	1137
Db	1084	AGTTTTCGGAATCTTCGGGTACTACTACCTTCAGATGAGAGAGCCGCTGTCTCAGCATTTCC	1143
Qy	1138	AGCGTCGCGAGCATCTT	1153
Db	1144	AGCGTCCGCGACACTT	1159

## RESULT 13

ID AAX59377 standard; cDNA; 1343 BP.

AC AAX59377

DT 20-SEP-1999 (first entry)

Rat EDG-7 receptor homologue cDNA.

KW EDG-7; rat; HEDG-7; G protein coupled receptor; asthma;

KW cardiac ischaemia; acute pancreatitis; septic shock; psoriasis;

Lung damage; diagnosis; therapy; drug screening;

22X  
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ET	
EY	2..682
CDS	/+22-

/partial  
EY  
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PN MO9935100-AZ.  
XX

PD  
XX

XX 30-DEC-1996: 98WC-CA01196.

XX 20-DEC-1951, 3105-00/0104.

(U) URGENT 0607Z APR 89  
FM JCRC  
TO DIA  
INFO SECDEF  
SUBJ: 1989-04-06 0607Z APR 89  
XX

XX  
F1  
cupca nn, mauloe oo, kastlawily kl,

DR P-PSDB: AAY06413.

PT A nucleic acid sequence encoding human EDG-7 receptor, useful for

[illegible][illegible]

a rat EDG-7 receptor homologue (see AAY06413). The

CC primers (see AAX59375-76) and primers based on mouse edq-7 sequences

CC HEDG-7 (see AY06411-12), a novel 7-transmembrane G protein coupled

diagnosis and proper treatment of abnormal conditions, e.g. adult

CC Ischaemia, acute pancreatitis, septic shock, psoriasis, acute

CC well as lung damage following exposure to cigarette smoke, asbestos

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Query Match	37.98;	Score 437.8;	DB 20,	Length 1343;
Best Local Similarity	78.68;	Pred. No. 7.9e-65;		
Matches 523; Conservative	0;	Mismatches 142;	Indels 0;	Gaps 0;

OY	480	CCGCGCTACGGCTTCATCGGCACTCTGTGGCGTGGCCGCGCTGGGGATCTGGCC	539
Db	1	CCGGTGTATGGCTCATCGATCGATCTGTCTGGCGCTGGAGCATCACTCGGGCTGTGGCC	60
OY	540	TTTGTGCGGGCTGGAGCTCCGCTGGCGCTTTTACCGCGTGTCCAGCTCTGTGGCCCTCTA	599
Db	61	CTCTGTGGCTGTGAACCTGTGTGTGGCTCTCCAGCGCTCTGTAGCTGTGGCCCTCTTA	120
OY	600	CTCCAAAGCGCTACATCTCTCTTCTCCCTGGGTATCTTCGCGGAGCTCTCTGGCCACATCAT	659
Db	121	CTCCAAAGGGCTATATGTGCTCTTTTGTGGTGGGTCTCTCCCTCACTCAATGTACGTATCTCT	180
OY	660	GGGCGCTCTTGGGGGCAATCTTCGCGCTGGGTGACAGCGACGGGAGAGAAAGGCCACAGGCC	719
Db	181	GAGCTCTTACGGGGGCATCTTTAGGGTGGTCCGAGGCCACAGGGCAGAAATCTCCCGGCTCC	240
OY	720	AGCGGCCCGCCGCAAGCGCCGCGCTGCTGAAGAGCGTGTATGATCTCTGTGGCTT	779
Db	241	TCTCGGCCCGCCAGATCTCCGCGAGCTATCTCAACACACGCTGTATGATCTGTGGCTTT	300
OY	780	CTGTGGTCTGGGGCCCACTCTCGGGGCGTGGCGTGGCCACACTCTTTTGGCTCAACT	839
Db	301	TGTGTGTCTGGGGTCCCTGTTTGGCTGTCCCTGGCCACATCTTTTGGATCTAATGT	360
OY	840	CTGGGGCCAGAGATCTCTGTGGGGGATGAGATGATCTGTGGCTCGGCTCTCTCACTC	899
Db	361	CTGGGGCCAGAGATCTCTGTGGGGGATGAGATGATCTGTGGCTCGGCTCTCTCACTC	420
OY	900	GGGCGTCAACCCATCATCTACTCTCTCCGACAGGAGAGGTGTGCAGAACCCCTGGCTCAG	959
Db	421	AGGATCATATCTCATCTATCTCTCTCCGACAGCGTGGTGCAGACGCTGTGTCAG	480
OY	960	CTTCTCTCTCTGGGGGTCTCTCCGGGTGGGCAATGGAGGGGCGCGGGAGCTGTGGCCCG	1019
Db	481	CTTCTCTCTCTGGGGGTCTCTCCGGGTGGGCAATGGAGGGGCGCGGGAGCTGTGGCCCG	540
OY	1020	GGCGGTGAGGCTCATCTCCGGAGTTCTCACACCGACAGCTCTCTGAGGCGCAAGGACAG	1079
Db	541	GATCACCGGAGGCGCACTCTGGGGGATCTCACACACTGACAGCTCTGCTGAGGCGCCAGGAAAG	600
OY	1080	CTTTCACGGGCTCCGCACTGTGCACCTTGTGGATGGGGGAGGCCCTGTGCAGATCTACCT	1139
Db	601	TTTTTCGACTTGTGAGTACCTACACTTCAAGATGAGAGAGCGGCTGTCCAGCTTTCCAG	660
OY	1140	CGTGC 1144	
Db	661	CATTC 665	

## RESULT 14

ID AAX36567 standard; DNA; 1137 BP.

AC AAX36567;

DT 07-JUL-1999 (first entry)

DE Human EDG-3 coding sequence.

KW EDG-1; EDG-2; EDG-3; EDG-4; EDG-5; PSP-24; human; detection; therapy;

KW LPA signalling mediated disease; cellular apoptosis; ss.

05 Homo sapiens

PN W09919513-A2

PD 22-APR-1999





comprising LPA modulators to the LPA or receptor. The method is useful for treating diseases characterised by slowed growth or repair of neuronal cells, neurodegenerative diseases, such as Alzheimer's disease, Parkinson's disease, and acute neuron damage, for modulating apoptotic pathways and treating ischemic heart disease, tumours, viral diseases CC bowel disease, and rejection of organ transplants.

XX Sequence 1137 BP; 226 A; 362 C; 298 G; 251 T; 0 other;

Query Match 22.28; Score 256; DB 22; Length 1137;  
Best Local Similarity 56.78; Pred. No. 2,2e-34;  
Matches 513; Conservative 0; Mismatches 385; Indels 6; Gaps 2;

OY 81 GCATACACACCTCGGGCCGCTGCGGGGCGGGGGGCGGAGGATGGCGCTGGG 140  
DB 60 GCATTACCAAGTACGTGGGGAAGTTGGGGGAGGCTGAGAGAGGCCCTCCGAGGGCAGAC 119  
OY 141 GGGCCCTGGGGGGGCTGTCGGTGGCGCCAGCTGCTGGTGGTGGAGAATTTGCTGT 200  
DB 120 GCTCACACCGTCTCTTCTGTCATCTGCAGCTTCATCTTGGAGAACCCTGATGT 179  
OY 201 GCTGGCGGCGCTACACAGCCATGCGGTCCGACGCTGGGTCTACTATTGCTGTGAA 260  
DB 180 TTTGATTTGCCATCTGGAAAAACAATAATTTCACACCGCATGTACTTTTCATTGGCAA 239  
OY 261 CATCACGCTGAGTACCTGCTCACGGGGGCGGCTTACCTGGCCAACTGCTGTGGG 320  
DB 240 CTTGCTCTCTGCGACCTGCTGGCGGGCATGCTTACAGGTCAACATTTGATGTCTGG 299  
OY 321 GGGCCGACCTTCGCTGCGGGCGGCGCCAGTGGTCTTACGGGAGGGCCTGCTTAC 380  
DB 300 CAAGAGACGTTTACAGCCGTCTCCACGGTCTGCTTCCAGGAGGGGCGATATGTCTGT 359  
OY 381 CGCCCTGGCGGCTCCACCTTACAGCTGCTTCTACTGCAAGGAGGAGGCTTGGCCACAT 440  
DB 360 GGGCCTTGGGGCTCCAGCTGAGCTTACCTGCGCATCGCATGCGGCACTTGACAT 419  
OY 441 GGTGGCGCGGCTGGCGGAGAGAGGCGGCGCCACCAAGACCGCGCTTACGCTTACATCG 500  
DB 420 GATCAAAATGAGGCTTA---CGAGGCCAACAGAGGACCGCGCTTCTCTCTGATCGG 476  
OY 501 CCTGTGCTGCTGCTGGCGCGGCTGCTGGGATGCTGCTTGTGGCTGGAAGTGTCT 560  
DB 477 GATGTGCTGCTCATTTGCTTACGCTGGGGCGGCTGCGCATTTCTGGCTGGAATGCTCT 536  
OY 561 GTGGCGCTTTACCGCTGCTCCAGCTTCTGCGCTTACTCCAAAGCGCTACATCTCTT 620  
DB 537 GCACATCTCCCTGACGTGCTTACCATCTGCGCTTACTCTCAAGAAGTACATGCTCTT 596  
OY 621 CTGCTGTGATCTTTCGCGCGGCTGCTGGCCACCATCATGCGGCTCTATGGGGCCATCTT 680  
DB 597 CTGCTATCAGCATCTTCAAGGCGCATCTGTGATCATGTCATCTTACGACGACATCTA 656  
OY 681 CCGCGTGTGACAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 740  
DB 657 CTTCCTGTGTAAGTCCAGCACCGCTAAGGTGCGCAACCAACTCGAGCGGTCCAT 716  
OY 741 CCGCTGTGTAAGGAGGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800  
DB 717 GGCATGTGCGGAGCGGCTGATGTGTGATGTGTGATGTGTGATGTGTGATGTGTGATGT 776  
OY 801 CTTCGCGCTGCTGCTGCGGAGCTTTCGCTTCCAACTCTGGGCCGAGAGTACTGCG 860  
DB 777 CTTCATCTCTTCTCATTTGATG---TGGCCTGAGGAGTGGAGGCGTGGCCCATCTCTT 833  
OY 861 GGGCATGAGTGTGATCTGCGGCTGCGGCTGCTCAACTGCGGCTCAACCCCATCATCTA 920  
DB 834 CAAGGCTCAGTGTTCATCTGTGTGCTGTCAACTCCGCAATGAACCGGATCATCTA 893  
OY 921 CTCCTTCCGACAGGAGGAGTGTGAGAGCGGTGCTCAAGTCTCCTGCTGCTGGGGTGTCT 980  
DB 894 CACGCTGGCAGAGAGAGATGGCGGGGCTTCTCCGCTGTGATGTGCAACTGCTGTGT 953

OY 981 CCGG 984  
DB 954 CAGG 957  
Search completed: December 13, 2002, 08:43:48  
Job time : 333 secs





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Db 1064 CTGGTGTGCGGGGCCACTCTTGCGGCTGCTGCGCCGACGTCCTTGGCCAACTTC 1123
QY 841 TGGGCCCGAGAGTACCTTCCGCGGAGATGAGATCTCTGGCCCTGCTCAACACG 900
Db 1124 TGGGCCCGAGAGTACCTTCCGCGGAGATGAGATCTCTGGCCCTGCTCAACACG 1183
QY 901 GCGGTCAACCCCATCATCTACTCTTCCGAGCAGGAGAGTGTGACAGACCGCTGCTCAGC 960
Db 1184 GCGGTCAACCCCATCATCTACTCTTCCGAGCAGGAGAGTGTGACAGACCGCTGCTCAGC 1243
QY 961 TTCTCTGCTGCGGGGTGCTCTCCGGCTGGGATGCGAGGCGCGGAGACTGCTGGCCCGG 1020
Db 1244 TTCTCTGCTGCGGGGTGCTCTCCGGCTGGGATGCGAGGCGCGGAGACTGCTGGCCCGG 1303
QY 1021 GCGGTCAAGGCTCACTCCGAGCTTCCACACCCAGACAGCTCTCTGAGGCCAAGGAGCAGC 1080
Db 1304 GCGGTCAAGGCTCACTCCGAGCTTCCACACCCAGACAGCTCTCTGAGGCCAAGGAGCAGC 1363
QY 1081 TTTCGCGGCTCCCGTGCCTGCTGCTTTCGAGATGCGGGAGCCCTGTCCAGCATCTCCAGC 1140
Db 1364 TTTCGCGGCTCCCGTGCCTGCTGCTTTCGAGATGCGGGAGCCCTGTCCAGCATCTCCAGC 1423
QY 1141 GTCCGAGACATCTGA 1155
Db 1424 GTCCGAGACATCTGA 1438

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RESULT 3
US-09-731-030A-10
; Sequence 10, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAMNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731, 030A
; PRIOR FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(1170)
US-09-731-030A-10

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Query Match 100.0%; Score 1155; DB 10; Length 2270;
Best Local Similarity 100.0%; Pred. No. 5, 2e-206;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAAGCCACGCGGAGCCCGGATGAGCCCGAGTCTGCCAACAGCTGCGCGCGGCGGG 60
Db 16 ATGAAGCCACGCGGAGCCCGGATGAGCCCGAGTCTGCCAACAGCTGCGCGCGGCGGG 75
QY 61 CAGAGCGGCTCATTTGCTGTGACACTACACACACTCGGCGCGGCTGGCCGGGCGGGGG 120
Db 76 CAGAGCGGCTCATTTGCTGTGACACTACACACACTCGGCGCGGCTGGCCGGGCGGGGG 135
QY 121 CCGGAGATGAGCGGCTGAGGGGCCCTGCGGGGCTGTGAGTGACCGCAACTGCTGAGTG 180
Db 136 CCGGAGATGAGCGGCTGAGGGGCCCTGCGGGGCTGTGAGTGACCGCAACTGCTGAGTG 195
QY 181 GTGCTGGAAGACTGTGCTGTGCTGGCGGCGCATTCACAGCCACATGCGGTCGCGACGCTGG 240
Db 196 GTGCTGGAAGACTGTGCTGTGCTGGCGGCGCATTCACAGCCACATGCGGTCGCGACGCTGG 255

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QY 241 GTCTACTATTCGCTGTGTAACATACGCTGAGTGAAGCTCTGTCACGAGGCGGAGCTTACCTG 300
Db 256 GTCTACTATTCGCTGTGTAACATACGCTGAGTGAAGCTCTGTCACGAGGCGGAGCTTACCTG 315
QY 301 GCCAAGCTGTGCTGTGTGGGGGCGGAGCTTCCGCTGTGGGCGCGGCCAATGAGTCTCTTA 360
Db 316 GCCAAGCTGTGCTGTGTGGGGGCGGAGCTTCCGCTGTGGGCGCGGCCAATGAGTCTCTTA 375
QY 361 CCGGAGGAGCTGCTTACCGCGGCTTCCAGCCGCTTCCAGCTTACGCTGCTTCACTGCA 420
Db 376 CCGGAGGAGCTGCTTACCGCGGCTTCCAGCCGCTTCCAGCTTACGCTGCTTCACTGCA 435
QY 421 GGGAGAGCTTTGCCACCATGTGTGCGGCGGCTGGCGGAGGCGGAGGCCAACAAGACAGC 480
Db 436 GGGAGAGCTTTGCCACCATGTGTGCGGCGGCTGGCGGAGGCGGAGGCCAACAAGACAGC 495
QY 481 CCGCTTACGCTTACATGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 496 CCGCTTACGCTTACATGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
QY 541 TTCTGCGGCTGGAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 600
Db 556 TTCTGCGGCTGGAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 615
QY 601 TCCAGAGCTTACATCTCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 660
Db 616 TCCAGAGCTTACATCTCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 675
QY 661 GGCCTTATAGGGGCACTTTCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 720
Db 676 GGCCTTATAGGGGCACTTTCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 735
QY 721 GCGGCGCCCGCAAGAGCGCGCGGCTGCTGAAGACGCTGATGATCTGCTGCTGCTGCTGCTGCT 780
Db 736 GCGGCGCCCGCAAGAGCGCGCGGCTGCTGAAGACGCTGATGATCTGCTGCTGCTGCTGCTGCT 795
QY 781 CTGGTGTGCTGGGCGGCACTTTCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 840
Db 796 CTGGTGTGCTGGGCGGCACTTTCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 855
QY 841 TGGGCCCGAGAGTACCTTCCGCGGAGATGAGATCTTGGCCCTGCGCTCTCTCAACTCG 900
Db 856 TGGGCCCGAGAGTACCTTCCGCGGAGATGAGATCTTGGCCCTGCGCTCTCTCAACTCG 915
QY 901 GCGGTCAACCCCATCATCTACTCTTCCGAGCAGGAGAGTGTGAGAGCGTGTGCTGACG 960
Db 916 GCGGTCAACCCCATCATCTACTCTTCCGAGCAGGAGAGTGTGAGAGCGTGTGCTGACG 975
QY 961 TTCTCTGCTGCGGGTGTCTCGGCTGGGATGCGAGGCGCGGAGCTGCTGGCCCGG 1020
Db 976 TTCTCTGCTGCGGGTGTCTCGGCTGGGATGCGAGGCGCGGAGCTGCTGGCCCGG 1035
QY 1021 GCGGTCAAGGCTCACTCCGAGGCTTCCACACCCAGACAGCTCTGAGGCGCAAGGAGCAGC 1080
Db 1036 GCGGTCAAGGCTCACTCCGAGGCTTCCACACCCAGACAGCTCTGAGGCGCAAGGAGCAGC 1095
QY 1081 TTTCGCGGCTCCCGTGCCTGCTGCTTTCGATGCGGAGGCGGCTGTCCAGACTTCCAGC 1140
Db 1096 TTTCGCGGCTCCCGTGCCTGCTGCTTTCGATGCGGAGGCGGCTGTCCAGACTTCCAGC 1155
QY 1141 GTCCGAGACATCTGA 1155
Db 1156 GTCCGAGACATCTGA 1170

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RESULT 4
US-09-731-030A-12
; Sequence 12, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAMNY, Roman L.

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```

; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; CURRENT FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1167)
US-09-731-030A-12

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Query Match          99.7%; Score 1151.8; DB 10; Length 1176;
Best Local Similarity 99.8%; Pred. No. 2e-205;
Matches 1153; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGAAGCCAGCGGGACCCCGTGGCCCGAGTCTGCGCAACAGCTGGGGCGGGGG 60
DB 13 ATGAAGCCAGCGGGACCCCGTGGCCCGAGTCTGCGCAACAGCTGGGGCGGGGG 72
QY 61 CACAGCCGGCTCATTTGTTCTGCACTACACACTGGGGCGGGCGGGGGGG 120
DB 73 CACAGCCGGCTCATTTGTTCTGCACTACACACTGGGGCGGGCGGGGGGG 132
QY 121 CCGAGAGATGGGGGCGTGGGGCGGCTGCGGGGCTGCGTGGCGCCAGTGGCTGTG 180
DB 133 CCGAGAGATGGGGGCGTGGGGCGGCTGCGGGGCTGCGTGGCGCCAGTGGCTGTG 192
QY 181 GTGCTGAGAAATTTCTGCTGCTGGGGCGGCATACAGCGCAATGGGTGGCGAGCTGG 240
DB 193 GTGCTGAGAAATTTCTGCTGCTGGGGCGGCATACAGCGCAATGGGTGGCGAGCTGG 252
QY 241 GTCTACTATTTGCTGCTGTAACATACAGCTGAGCTTCTACAGGGGGGCTTACTTG 300
DB 253 GTCTACTATTTGCTGCTGTAACATACAGCTGAGCTTCTACAGGGGGGCTTACTTG 312
QY 301 GCCAAGTGTCTGCTGCGGGGGCGGACCTTCCGTCTGGCGCCGCCCAATGGTTCCTA 360
DB 313 GCCAAGTGTCTGCTGCGGGGGCGGACCTTCCGTCTGGCGCCGCCCAATGGTTCCTA 372
QY 361 CCGGAGAGGCTGCTTCTTACAGCGCCCTGGCGCTTCCACTTACGCTTCTTACTGCA 420
DB 373 CCGGAGAGGCTGCTTCTTACAGCGCCCTGGCGCTTCCACTTACGCTTCTTACTGTA 432
QY 421 GGGGAGCGCTTTGCCACCATGTCGGCGCGTGGCGGAGCGGGGCCACCAAGACCAGC 480
DB 433 GGGGAGCGCTTTGCCACCATGTCGGCGCGTGGCGGAGCGGGGCCACCAAGACCAGC 492
QY 481 CGGGCTACAGGCTTACAGGGGCTGCTGCTGGCTGCTGGCGGGCTGCTGGGGAGTCTGCT 540
DB 493 CGGGCTACAGGCTTACAGGGGCTGCTGCTGGCTGCTGGCGGGCTGCTGGGGAGTCTGCT 552
QY 541 TTGCTGAGGCTGAGACTGCTGCTGCGCTTTGACCGCTGCTCCAGCTTCTGCGCCCTTAC 600
DB 553 TTGCTGAGGCTGAGACTGCTGCTGCGCTTTGACCGCTGCTCCAGCTTCTGCGCCCTTAC 612
QY 601 TCCAGAGCGCTACATCTTCTGCGCTGATCTTGGCGGCGTGGCTGCGGACCATCATG 660
DB 613 TCCAGAGCGCTACATCTTCTGCGCTGATCTTGGCGGCGTGGCTGCGGACCATCATG 672
QY 661 GGGCTCTAAGGGGCGCATCTTCCGCGCTGTCAGAGCGAGGGGCAAAAGCCCGCAGCCCA 720
DB 673 GGGCTCTAAGGGGCGCATCTTCCGCGCTGTCAGAGCGAGGGGCAAAAGCCCGCAGCCCA 732
QY 721 GCGGCGCGCGCGCAAGCGCGCGCGCTGCTGAAGACGGTCTGATGATCTGCTGGCCTTC 780
DB 733 GCGGCGCGCGCGCAAGCGCGCGCGCTGCTGAAGACGGTCTGATGATCTGCTGGCCTTC 792

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QY 781 CTGATGTGCTGGGGGCCACCTCTTGGGGCTGCTGCGGCGGAGCTCTTGGCTCCAACTC 840
DB 793 CTGATGTGCTGGGGGCCACCTCTTGGGGCTGCTGCGGCGGAGCTCTTGGCTCCAACTC 852
QY 841 TGGGCCAGAGTACTTGGGGGCGGAGTGGATCTTGGCCCTGGCGCTTCACTCG 900
DB 853 TGGGCCAGAGTACTTGGGGGCGGAGTGGATCTTGGCCCTGGCGCTTCACTCG 912
QY 901 GCGGTCAACCCCATCTACTTCTTCCGAGCAGAGGAGTGTGACAGCGCTCTCAGC 960
DB 913 GCGGTCAACCCCATCTACTTCTTCCGAGCAGAGGAGTGTGACAGCGCTCTCAGC 972
QY 961 TTCTCTGTGCTGGGGTGTCTTCCGGCTGGGATGTCAGAGGGCCCGGGGAGTGGCTGG 1020
DB 973 TTCTCTGTGCTGGGGTGTCTTCCGGCTGGGATGTCAGAGGGCCCGGGGAGTGGCTGG 1032
QY 1021 GCGGTGAGGCTCACTCCGGAATTCACCCAGCAGACGCTCTGAGGCCAAGGAGACG 1080
DB 1033 GCGGTGAGGCTCACTCCGGAATTCACCCAGCAGACGCTCTGAGGCCAAGGAGACG 1092
QY 1081 TTTCGGGGCTCCCGCTGCTGAGCTTTCGATGCGAGGAGCCCTGCTCCAGCATCTCAGC 1140
DB 1093 TTTCGGGGCTCCCGCTGCTGAGCTTTCGATGCGAGGAGCCCTGCTCCAGCATCTCAGC 1152
QY 1141 GTGCGGAGCATCTGA 1155
DB 1153 GTGCGGAGCATCTGA 1167

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RESULT 5
US-09-731-030A-14
; Sequence 14, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; PRIOR FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-731-030A-14

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Query Match          99.5%; Score 1148.8; DB 10; Length 1152;
Best Local Similarity 99.8%; Pred. No. 7.1e-205;
Matches 1150; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGAAGCCAGCGGGACCCCGTGGCCCGAGTCTGCGCAACAGCTGGGGCGGGGG 60
DB 1 ATGAAGCCAGCGGGACCCCGTGGCCCGAGTCTGCGCAACAGCTGGGGCGGGGG 60
QY 61 CACAGCGGCTCATTTGTTCTGCACTACACACTGGGGCGGGCGGGGGGG 120
DB 61 CACAGCGGCTCATTTGTTCTGCACTACACACTGGGGCGGGCGGGGGGGGG 120
QY 121 CCGGAGAGTGGGGGCGTGGGGGCGGCTGCGGGGCTGCTGGGGCGGCAAGTGTGCTGGTG 180
DB 121 CCGGAGAGTGGGGGCGTGGGGGCGGCTGCGGGGCTGCTGGGGCGGCAAGTGTGCTGGTG 180
QY 181 GTGCTGAGAACTTGTGCTGCTGGGGCGCATACAGCGCAATCGGTGCGGAGCTGG 240
DB 181 GTGCTGAGAACTTGTGCTGCTGGGGCGCATACAGCGCAATCGGTGCGGAGCTGG 240
QY 241 GTCTACTATTTGCTGCTGTAACATACAGCTGAGTGAAGCTGCTCAGCGGGGCGGCTTACTTG 300
DB 241 GTCTACTATTTGCTGCTGTAACATACAGCTGAGTGAAGCTGCTCAGCGGGGCGGCTTACTTG 300

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Dh	241	GTCTACTATTTGGCTGTGGTGAACATCAACGCTGATGATACCTGCTCAAGGGGCGGGCCCTACTCTG	300
Oy	301	GCCAAAGCTGCTGTGTGTGGGGGGGCGCCGACACTTTCGGTCTGGGCGCCGCCCAAGTGTTCCTA	360
Dh	301	GGCAACAGTGTGTGTGTGGGGGGGCGCCACCTTTCGGTCTGGGCGCCGCCCAAGTGTTCCTA	360
Oy	361	CGGGAGGGGCGTGTCTTTCACCGGCCCTGGGCGCGCTTCACACTTTCACAGCCGTCTTTCACGTCA	420
Dh	361	CGGGAGGGGCGTGTCTTTCACCGGCCCTGGGCGCGCTTCACACTTTCACAGCCGTCTTTCACGTCA	420
Oy	421	GGGGAGGCGCTTTCGACCAATAGTGTGGGGCGGGGCGGAGCCGAGAGCGGGGCGACCAAGACCAAGC	480
Dh	421	GGGGAGGCGCTTTCGACCAATAGTGTGGGGCGGGGCGGAGCCGAGAGCGGGGCGACCAAGACCAAGC	480
Oy	481	CGGCTCTACGCGCTTCATCGGCGCTCTGTGTGGCTGTGTGGCGCGGCGCTGTGTGGGGATGCTGCCT	540
Dh	481	CGGCTCTACGCGCTTCATCGGCGCTCTGTGTGGCTGTGTGGCGCGGCGCTGTGTGGGGATGCTGCCT	540
Oy	541	TTTGCTGGGCGTGAACACTCGCTGTGCGGCGTTCGACGCGTTCGACAGCCGTTCGCGCCCTTAC	600
Dh	541	TTTGCTGGGCGTGAACACTCGCTGTGCGGCGTTCGACGCGTTCGACAGCCGTTCGCGCCCTTAC	600
Oy	601	TCCAAAGCGTCAATCTCTCTCTGT	660
Dh	601	TCCAAAGCGTCAATCTCTCTCTGT	660
Oy	661	GGGCTCTATGAGGGGCGCATCTTTCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720
Dh	661	GGGCTCTATGAGGGGCGCATCTTTCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720
Oy	721	GGGCGCGCGCGCGAAGGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
Dh	721	GGGCGCGCGCGCGAAGGCGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
Oy -	781	CTGT	840
Dh	781	CTGT	840
Oy	841	TGGGCGCAAGAGTACCTGTGGGGGGCATGTGACTGGATCTGTGGCGCCGTGGCGCTCTCAACTCG	900
Dh	841	TGGGCGCAAGAGTACCTGTGGGGGGCATGTGACTGGATCTGTGGCGCCGTGGCGCTCTCAACTCG	900
Oy	901	GGCGTCAACCCCATCATCTACTCTCTTCCGACACAGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT	960
Dh	901	GGCGTCAACCCCATCATCTACTCTCTTCCGACACAGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT	960
Oy	961	TTTCTCTGT	1020
Dh	961	TTTCTCTGT	1020
Oy	1021	GGCGTGAAGGCTCACTCGGAGGCTTCACACACGACGACCTCTGTGAAGGCGMAAGGACAGC	1080
Dh	1021	GGCGTGAAGGCTCACTCGGAGGCTTCACACACGACGACCTCTGTGAAGGCGMAAGGACAGC	1080
Oy	1081	TTTTCGGGCGT	1140
Dh	1081	TTTTCGGGCGT	1140
Oy	1141	GTGCGGAGCATC 1152	
Dh	1141	GTGCGGAGCATC 1152	
RESULTS			
US-09-827-937A-3			
: Sequence 3A, Application US/09827937A			
: Patent No. US20020052043A1			
: GENERAL INFORMATION:			
: APPLICANT: LI, YI			
: APPLICANT: Ruden, Steven M.			
: TITLE OF INVENTION: Human G-Protein Coupled Receptors			
: FILE REFERENCE: 1488.120003			
: CURRENT APPLICATION NUMBER: US/09/827,937A			

[illegible]

QY 841 TGGGCCAGAGTACCTGCGGGGCGATGAGTGGATCTGGCCCTGGCCCTTCACATCG 900  
DB 890 TGGGCCAGAGTACCTGCGGGGCGATGAGTGGATCTGGCCCTGGCCCTTCACATCG 949  
QY 901 GCGGTCAACCCCATCATCTACTCTCTCCGACAGAGAGGTGTGACAGCCGTCTAGC 960  
DB 950 GCGGTCAACCCCATCATCTACTCTCTCCGACAGAGAGGTGTGACAGCCGTCTAGC 1009  
QY 961 TTCTCTGTCTGCGGGGTGTCTCCGGCTGGGCGATGCGAGGGCCCGGGGACTGCTTGGCCCG 1020  
DB 1010 TTCTCTGTCTGCGGGGTGTCTCCGGCTGGGCGATGCGAGGGCCCGGGGACTGCTTGGCCCG 1069  
QY 1021 GCGGTCAAGGCTCACTCCGAGGCTTCCACACGACGACGCTCTGAGGSCAAAGGACAGC 1080  
DB 1070 GCGGTCAAGGCTCACTCCGAGGCTTCCACACGACGACGCTCTGAGGSCAAAGGACAGC 1129  
QY 1081 TTTTGGGGGCTCCGCTCGCTCAGCTTTGGGATGCGGAGCCCTGTCCAGCATCTCCAGC 1140  
DB 1130 TTTTGGGGGCTCCGCTCGCTCAGCTTTGGGATGCGGAGCCCTGTCCAGCATCTCCAGC 1189  
QY 1141 GTGCGGAGCATCTGA 1155  
DB 1190 GTGCGGAGCATCTGA 1204  
RESULT 7  
US-09-917-508-1  
; Sequence 1, Application US/09917508  
; Patent No. US20020137136A1  
; GENERAL INFORMATION:  
; APPLICANT: TSUI, Ping  
; TITLE OF INVENTION: Rat G Protein Coupled Receptor, ED65  
; FILE REFERENCE: GP-70715  
; CURRENT APPLICATION NUMBER: US/09/917, 508  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1161  
; TYPE: DNA  
; ORGANISM: RAT  
US-09-917-508-1  
Query Match 65.28; Score 752.8; DB 10; Length 1161;  
Best Local Similarity 79.4%; Pred. No. 1,6e-131;  
Matches 918; Conservative 0; Mismatches 232; Indels 6; Gaps 2;  
QY 1 ATGAAGCCACGAGGAGCCCGGTTGCGCCGAGTCTTGCCACAGCTGGCGCGGCG 60  
DB 7 ATCAGTACTGTGTCACGATGAGTACCCAGAGTCTTGCCACGAGCTGGCGCGGCGT 66  
QY 61 CACAGCCGCTCATTTCTTGACACTACAAACACTGCGGCGCGGCTGGCGGCGCGG 120  
DB 67 CACAGCCGCTCATTTCTTGACACTACAAACACTGCGGCGCGGCTGGCGGCGCGG 126  
QY 121 CCGGAGG---ATGCGGCGCTGCGGGGCTGTGCGGGGCTGTGCGGCGCGGCGGCT 177  
DB 127 CCGGAGG---ATGCGGCGCTGCGGGGCTGTGCGGGGCTGTGCGGCGCGGCGGCT 186  
QY 178 GTGGTGTGAGGAAGT 237  
DB 187 GTGGTGTGAGGAAGT 246  
QY 238 TGGGTCTACTATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 297  
DB 247 TGGGTCTACTATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 306  
QY 298 CTGGGCAACGCTGT 357  
DB 307 GTGGTCAACGCTGT 366

QY 358 CTACGAGAGGCGCTGCTCTTACACCGCCCTTGCGCGGCTTCACCTTACAGCTGTCTACT 417  
DB 367 CTGGGGAGAGGCGCTGCTCTTACATGAGGCGCGCTGCGCTGCGCTACCTTACATCTTAC 426  
QY 418 GCAGGGAGAGGCGCTTTCGACATGAGTGTGCGGCGGTGTGCGGAGAGCGGCGACCAAGAC 477  
DB 427 GCGGAGAGAGGCGCTTTCGACATGAGTGTGCGGCGGTGTGCGGAGAGCGGCGACCAAGAC 483  
QY 478 AGCGGCTCTACAGGCTTACATCGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 537  
DB 484 AGCGGCTCTACAGGCTTACATCGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 543  
QY 538 CCTTGT 597  
DB 544 CCTTGT 603  
QY 598 TACTTCAGAGGCTTACATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657  
DB 604 TACTTCAGAGGCTTACATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 663  
QY 658 ATGGGCTCTATGAGGCGCATCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 717  
DB 664 CTGAGCTCTACGAGGCGCATCTTATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 723  
QY 718 CCAAGGAGCGCGCGCGCAAGGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 777  
DB 724 CCGCTGT 783  
QY 778 TTCTGT 837  
DB 784 TTCTGT 843  
QY 838 CTGTGGGCGGAGAGTACCTGTGCGGCGCATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 897  
DB 844 GTCTGGGCGGAGAGTACCTGTGCGGCGCATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 903  
QY 898 TCGCGGCTCAACCCCATCATCTCTCTTCCGACAGAGGAGTGTGTGTGTGTGTGTGTGT 957  
DB 904 TCACGCACTCATCTCTCATCTATCTCTTCCGACAGCGCTGTGTGTGTGTGTGTGTGTGT 963  
QY 958 AGCTTCTGT 1017  
DB 964 AGCTTCTGT 1023  
QY 1018 GCGGCGGTGAGAGTCACTCCGAGGCTTCCACACGACGACGCTCTGTGAGGCGCAAGGAG 1077  
DB 1024 GCGATCACCGAGGCGCATCTGTGGGCGATCCACACGACGCTGTGTGTGTGTGTGTGTGT 1083  
QY 1078 AGCTTGTGCGGCTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1137  
DB 1084 AGCTTGTGAGACTTGT 1143  
QY 1138 AGCGTGGGAGCATCT 1153  
DB 1144 AGCATCCGACGCGCT 1159  
RESULT 8  
US-09-731-030A-20  
; Sequence 20, Application US/09731030A  
; Patent No. US20020142375A1  
; GENERAL INFORMATION:  
; APPLICANT: MURROE, Donald G  
; APPLICANT: GUPTA, Ashwani K.  
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS  
; FILE REFERENCE: 8074-0015  
; CURRENT APPLICATION NUMBER: US/09/731,030A  
; PRIOR FILING DATE: 1998-12-29  
; PRIOR APPLICATION NUMBER: 60/070,184  
; NUMBER OF SEQ ID NOS: 21



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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1343
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(673)
; OTHER INFORMATION: "n" is residue 1325; "n" represents to C, T, G, or A
US-09-731-030A-20
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Query Match          37.9%; Score 437.8; DB 10; Length 1343;
Best Local Similarity 78.6%; Pred. No. 3.6e-73;
Matches 523; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
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QY 480 CCGGCTCTACGGCTTCATCGGCTCTGCTGGCTGCTGGCCGGCTGCTGGGATCTGCC 539
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CCGTGTGATGGCTGATGCTGTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCC 60
QY 540 TTTGCTGGGCTGGAACCTGCTGGCCCTTTGACCGCTGCTGACGCTTCTGACGCTTCTGAC 599
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CTTGCTGGGCTGGAACCTGCTGGCCCTTTGACCGCTGCTGACGCTTCTGACGCTTCTGAC 120
QY 600 CTCGAAGCCCTACATCTCTCTGCTGGCTGATCTTCCGGGCGCTGCTGGCCACCATCAT 659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CTCGAAGGCTATGCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 660 GGGGCTCTATGGGGCATCTTCCGCTGCTGTCAGGCGCAGCGGGGAGAAAGCCCGACGCC 719
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GAGCCTCTATGGGGCATCTTCTGCTGGCTGATCTTCCGGGCGCTGCTGGCCACCATCAT 240
QY 720 AAGGCGCCCGCCCAAGGCGCCGCGCTGCTGAAGAGGCTGATGATCTGCTGGCTT 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 TCTGCTGGCGCCCGCAAGTCTCCGCAAGCTACTCAACCGCTGATGATCTTGTGTGTGT 300
QY 780 CCTGCTGCTGGGGCCCACTCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 TGTGCTGCTGCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 840 CTGGGCGCCAGAGTACCTGCGGGGGGATGAGTACGATCTGCGGGCGCGCGCTGCTGCT 899
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CTGGGCGCCAGAGTACCTGCGGGGGGATGAGTACGATCTGCGGGCGCGCGCTGCTGCT 420
QY 900 GGGGCTCAACCCCATCATCTCTCTTCCGCAAGGAGGTGTGTCAGAGCCGCTGCTGAG 959
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 AGCATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 960 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1019
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 1020 GGGCGTGAAGGCTCACTGCGGAGCTTCCACACCGCAGCTCTCTGAGGCGCAAGGAGAG 1079
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GATCACCGAGGCGCTCTGCGGGGATCAACACCTGACACCTGCTGAGGCGCAAGGAGAG 600
QY 1080 CTCTGCGGCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 TTTTGGAGCTTGAGGCTACTCATGCTTCAAGATGAGAGCGCGCTGTCTCAGGCTTCCAG 660
QY 1140 CGTGC 1144
    |||
Db 661 CATGC 665
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RESULT 9
US-10-037-616-3
; Sequence 3, Application US/10037616
; Patent No. US20020123148A1
; GENERAL INFORMATION:
; APPLICANT: English, Denis
; APPLICANT: Kovacs, Richard J.
; APPLICANT: Rizzo, Maria T.
; APPLICANT: Silva, Daniel T.
```

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; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
; FILE REFERENCE: 7042-119
; CURRENT APPLICATION NUMBER: US/10/037,616
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/243,887
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1137)
; OTHER INFORMATION:
US-10-037-616-3
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Query Match          22.2%; Score 256; DB 12; Length 1137;
Best Local Similarity 56.7%; Pred. No. 1.7e-39;
Matches 513; Conservative 0; Mismatches 385; Indels 6; Gaps 2;
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QY 81 GCATACACCATCTCGGCGCGCTGCGCGGCGCGGCGCGGCGCGGAGATGCGGCGCTGG 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 GCATACACCATCTCGGCGCGCTGCGCGGCGCGGCGCGGCGCGGAGATGCGGCGCTGG 119
QY 141 GGGCCTGCGGGGCGCTGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCT 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 GCTACACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 179
QY 201 GCTGCGCGCATCAACGACCATGCGGCTGCGGCGCGGCGCGGCGCGGCGCGGCTGCTG 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 TTTGATGTCATCTGGAAGAAATTAATTTACACACCGCATGATCTTTTCAATGGCAA 229
QY 261 CATACGCTGATGATCTGCTCTACGCGCGCGGCGGCTTACCTGGCCACGCTGCTGCGG 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 CTTGCTCTCTGCGACCTGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 299
QY 321 GGGCGCGCATCTCTGCTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 CAAGAGACGTTCAAGCTCTGCTCTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
QY 381 CGCCCTGGCGCGCTCAACCTTCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 GGGCCTTGGGCGGCTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
QY 441 GGTGCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 420 GATCAAAATGAGGCGCTTA--CGAGGCGCAACAGAGGCGGCGGCGGCTCTCTCTGATCG 476
QY 501 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
QY 561 GTGCGCTTTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 GCACATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596
QY 621 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 CTGATCAAGCATCTTCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
QY 681 CCGGCTGCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 740
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 657 CTCTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
QY 741 CGGCTGCTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 800
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 GGCATCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 776
QY 801 CTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 860
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 777 CTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 833
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QY	861	GGGCATGACATCGATCCTGGSCCCTGGCCGTCCTAACTCGAGGTCACAACCCATCATCTA	920
Db	834	CAGAAGCTACAGGTTCATCGTGTGGCTGTGCCTCAACTCGGCATGAACCCGGTCATCTA	893
QY	921	CTCCTTCCGACAGAGGAGGTGTGCACAGGCCGTCTACGTTCTCTTGCTGGCGGTCTCT	980
Db	894	CACGCTGGCCAGCAAGGAGATGCGCGGCGCTTCTTCCGCTGTGATTGCACAACTCCGTGT	953
QY	981	CCGG	984
Db	954	CAGG	957

```

RESULT 10
US-09-842-316-1
: Sequence 1, Application US/09842316
: Patent No. US2002009191A1
: GENERAL INFORMATION:
: APPLICANT: KOSTENIS, Eva
: APPLICANT: GASENHEBER, Johann
: TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
: FILE REFERENCE: 38005-147
: CURRENT APPLICATION NUMBER: US/09/842,316
: CURRENT FILING DATE: 2001-04-26
: PRIOR APPLICATION NUMBER: EP 116589.3
: PRIOR FILING DATE: 2000-08-01
: PRIOR APPLICATION NUMBER: EP 108858.2
: PRIOR FILING DATE: 2000-04-26
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 1197
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1194)
: OTHER INFORMATION:
US-09-842-316-1

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Db	553	ACGTCCTTGCGCGCTATACGGCAGAGGCTACAGTGCCTCTCTGCGTCCGCTTCGCGCTTCGCGGCT	712
Qy	643	GTCTCTGGCCACCATCATATGGGCTCTATATGGGSCATCTTCGCGCTGGTGTGACAGCCAGCGG	702
Db	713	ATCTGGGCGCGCTATCTGTGACACTCTACGCGCCATCTACCTCCACAGGTACGCGCCCAACGCG	772
Qy	703	CAGAA-----GGCCCCACGCCAGGCGCGCCGCAAG	735
Db	773	CGCGCGCTGCGGACGCGCCGGAGCTGGGGGAGCACTGCACCGCGGCGGTGCGCAAG	832
Qy	736	GGCCGCG-----GCGTGGCAGAGCGGTGATGATCCGTCGCGGCGCTTCGCGGTGCG	789
Db	833	CGCGCGCTGCGTGGCGCTTGTGTGCGACGCTCAGACGTGTGTGCTCTGTGGCTTTTGTGGCATGT	892
Qy	790	TGGGGCCCACTCTTCGCGGCTGTGTGTGCGCGACGCTTTTGGCTTCAACCTCTGGGCCAG	849
Db	893	TGGGGGCGCCCTCTCTCGCTGTGTGTGTGTGCTGACGTGGCGGTGCTCCCGGCGGCGACCTGTGCTCT	952
Qy	850	GAGTACCTGTGCGGGGACATGAGACTGGATCTCGGCGCCGTGGCGCTCTCAACTGTGGGCGTTCAC	909
Db	953	GTACTCTGTGAGGCG---GATCCCTTCCGTGGAGCTCGGCGCATATGGCGCAACTACTTGTGAA	1009
Qy	910	CGCATCATCTACTCTCTTCCGCGACGAGGAGGTGTGCAAGCGCTGTCTCACTTCTCTTGTG	969
Db	1010	CCCATATCTATACGCTCTACCAACCGCGACTGTGCGCCACGCGGCTCTCTGCGCGCTGTGTGTG	1069
Qy	970	TGCGGATGTCTCGGCTGGGACATGACGAGGCGCCGGGAGCTGCTGTGGCGCGGCGCTCTCAG	1029
Db	1070	TGCGAGACGCGACTCTCTCGGCGCAGAGACCGAGTGTGCTCCGACGTCGTGGGAGCGCGGCT	1129
Qy	1030	GCCTACTCGGAGGTCTCCACACGACGACACTCTCTGAGAGGCCAAGGAGCAAGCTTGTGCGGCG	1089
Db	1130	GAGGCTTCCGGGGGCTGCGCGCTGTCTGCTGCGCGCGGCTTGTATGGAGACTTCAAGCGCG	1189
Qy	1090	TC 1091	
Db	1190	TC 1191	

```

RESULT 13
US-09-993-844-14
: Sequence 14, Application US/09993844
: Patent No. US20020106739A1
: GENERAL INFORMATION:
: APPLICANT: Oakley, Robert H.
: APPLICANT: Barak, Lawrence S.
: APPLICANT: Laporte, Stephane A.
: APPLICANT: Caron, Marc G.
: TITLE OF INVENTION: Modified G-Protein Coupled Receptors
: FILE REFERENCE: 033072-026
: CURRENT APPLICATION NUMBER: US/09/993, 844
: CURRENT FILING DATE: 2001-11-05
: PRIOR APPLICATION NUMBER: US 60/245,772
: PRIOR FILING DATE: 2000-11-03
: PRIOR APPLICATION NUMBER: US 60/260,363
: PRIOR FILING DATE: 2001-01-08
: NUMBER OF SEQ ID NOS: 81
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 1089
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: nucleotide sequence of Edg1-V2R chimera
: US-09-993-844-14

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Query Match	20.9%	Score 241.2;	DB 10;	Length 1089;
Best Local Similarity	54.6%;	Pred. No. 9,4e-37;		
Matches 586; Conservative	0;	Mis. 458;	Indels 30;	Gaps 4.

  

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OY      *ATGACAGCCACGGGGAACCCCGGTGGCCCCCGCAGTCTGCCCAACACTTGCGCGCGCGCGG 60
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D	b	1	ATGGGGCCACCAAGGCTCCCGCTGTGTAAGGCCACCGAGCTGGGTCTGTACTACATC	60
O	y	61	CACAGCCGGCTATTGTTCTCTACATACACCACTCGGGCGGGTGGCGGGGGGG	120
D	b	61	AACTATGATATATGTCGGGCACTTACACATACAGGAAAGCTGAATATACCGGGGAC	120
O	y	121	CCGAGAGATGGGGGCTGGGGGCCCTCGGGGGGTGTGAGGGCGGCACTGCTGTG	180
D	b	121	AAGGAACAGCATTAACCTAGC---TGGTGTTCATTTCACTGCTCTTATC	177
O	y	181	GTGTGAGAACCTTCTGCTGTGGGGGGCCATACAGACGACATGGCGTGGACGCTGG	240
D	b	178	ATCTGGAGAACATCTTGTCTTCTGACCATTTGGAAACCAAAATTCACGACCC	237
O	y	241	GTCTACTATTCCTGGTGAACATCAGCTAGTACCTCTACGGGGCGGCTACTG	300
D	b	238	ATGTACTATTTATTTAGGCAATCTGGCCCTCTCGACACTGTGGAGAGATGACTACAA	297
O	y	301	GCAACGTCCTCTTCGCGGGGGCCCGGACCTTCGCGTGGCGGGCCAGTGGTCTTA	360
D	b	298	GCTAACCTCTCTTGTCTGCGGGCCACCACTCAAGCTACCTCCGGCCAGTGTTCG	357
O	y	361	CGGAGAGGCTCTCTTACCGGCTCTGGCGGCTCTCACTTCAGCTGCTTTCATGTGA	420
D	b	358	CGGAAAGGAGATATTTGTGGCCCTGTACGCTCTGTTTACGTCTCTCGCAATGGC	417
O	y	421	GGGAGACGCTTGGCCACCATGTGTGGCGGTGGCGGAGCGGGGGCCACCAAGACAC	480
D	b	418	ATTGACGCTATATACATCTGTAATAATGAATCAACACGGG---AACCATTAATCTC	474
O	y	481	CGGTCTAGGCTATATAGGCTCTGCTGTGGCTGTGGCGCGGCTGGGAGATGAGCT	540
D	b	475	CGGCTTCTCTCTAATAGAGGCTGTGTGGTATCTCCATCATCTGGGTGGGCTGCT	534
O	y	541	TTCCTGGCTGGAATCTGCTGTGCGCTTTGACCGTGTCCAGCTTCTGGCCCTTAC	600
D	b	535	ATCATGGGCTGGAATGTGATAGTGGCGCTGTCACTGCTCCACGTTGGCGCTTAC	594
O	y	601	TCCAAACGCTAACATCTTCTGTGCTGTGATATCTGCGGCGTCTGGGCAACATCAG	660
D	b	595	CACAACCACTATATCTCTTCTGTGCACAGGCTTACATCTGTTGCTCTCATCTGC	654
O	y	661	GGCTGTATGGGGCCATTTCTCGGCTGTGAGAGGCGACGGGGCAGAAAGGCCACGCCCA	720
D	b	655	ATTCTGTACTGCAAGATTTACTCTTGTGTAGAGACTCGAGACCGCGGCTGACGTTCCG	714
O	y	721	GGGCGCCCGSCAAGGCGCCGCGC-----CTGTGAAGACGGT	759
D	b	715	AAGAAATTTTCCAAAGCGCACCGGAGCTGTGAAGATGCTGCGGCTGTCAAAACCTGA	774
O	y	760	CTGATGATCTCTGAGCTTCTGTGTGTGTGAGGGGACCACTTCTGGGCTGTGATGGGC	819
D	b	775	ATTATGTCGTAGAGGTTCTATGAGCTGTGGCGACCGGCTTTCATCTGCTCTGCG	834
O	y	820	GAGCTTTGTGCTCAACCTCTGGGCGCAAGATACATGCGGGGCAATGAGATCTCG	879
D	b	835	GATG---TGGGCTGAAGGTAAAGACCTGTGAATCTTTCACAGGGAATCTTCTCG	891
O	y	880	GCCCTGGCGCTCACTCACTGGCGGTCGAACCCCATCATCTACTCTTCCGACAGAGAG	939
D	b	892	GTTTATGCTGTCACTCACTCGGACCAACCCATCATTTACATCTGACCAACAAGAG	951
O	y	940	GTTGTGAGAGCGGTCTAGATTTCTGTGCTGTGGGGGTCTGCGGGTGGCATAGAGG	999
D	b	952	ATTCGTCGGGCTTTCATCTCGAATATGTCTCTGTCAAGTGGCGGCGCAGCGGAGCC	1011
O	y	1000	CCGGGGAATGCTCTGGCGCGGGCGTGAAGCTCACTCCGAGCTTCAACAC	1053
D	b	1012	ACCCCAACCGAGCTGGGTCCCAAGATGAGTCTGTACACACCGACACTCTTC	1065

RESULT 14  
US-09-971-228-2

```

; Sequence 2, Application US/09971228
; Patent No. US2002015512A1
; GENERAL INFORMATION:
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Esteban
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Jorge
; APPLICANT: Li, Congfen
; APPLICANT: Zhao, Haoran
; APPLICANT: Jiang, Yingping
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Edg: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310US
; CURRENT APPLICATION NUMBER: US/09/971,228
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/284,763
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: mutant #1, C-terminally truncated variant of
; OTHER INFORMATION: human endothelial differentiation G-protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(1031)
; OTHER INFORMATION: mutant #1 human EDG1
US-09-971-228-2

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Query Match      20.6%; Score 237.4; DB 9; Length 1032;
Best Local Similarity 55.7%; Pred. No. 4.7e-36;
Matches 554; Conservative 0; Mismatches 411; Indels 30; Gaps 4;

QY 1 ATGAAGCCACGGGAGACCCCGGTGGCCCGAGTCTGCAACACAGTGGCGCGCGG 60
DB 9 ATGGGGCCACCCAGCGTCCCGCTGGTCAAGGCCACCGAGCTGGTCTGACACGTC 68
QY 61 CACAGCGCGCTCATGTTCTGTGACATACACCACTGGGCGCGCTGGCGCGCGG 120
DB 69 AACTATGATATATGTCGCGGATTACACATACAGGAAACCTGAATATCAGCGCGAC 128
QY 121 CCGGAGGATGCGGGGCTGGGCGCTGGCGGGCTGGCGCGCGCGCGCTGGTG 180
DB 129 AAGGAGAACAGCATTAACCTGACC---TCGGTGGTGTTCATTTCTCATCTGCTTTATC 185
QY 181 GTGCTGAGAACCTGCTGTGCTGGCGGCATACACAGCCACATGCGGTGCGAGCGTGG 240
DB 186 ATCTGAGGAAACATCTTGTCTGTGCTGACCATTTGGAAACCAAGAAATTCACCGACCC 245
QY 241 GTCTACTATGCTGCTGTGAACATCAACGCTGAGTGAACCTGCTCAAGCGCGCGCTACCTG 300
DB 246 ATGTACTATTTTATTTGGAATCTGGCCCTGCTCAGACCTGTTGGAGAGGAGCTTACACA 305
QY 301 GCCAACGCTGCTGCTGCTGGGGGCGCCACCTTCGCTGGCGCGCGCGCGCGCTGCTCTA 360
DB 306 GCTAACGCTGCTGCTGCTGGGGGCGCCACACCTACACAGCTCATCCCGCCCAATGGTTTCTG 365
QY 361 CCGGAGGCGCTGCTTACACGCGCGCTGGCGCGCTTCACCTTCAGCTGCTTTCACAGCA 420
DB 366 CCGGAGGAGAGTATGTTGTGTGGCCCTGTCAGGCTCCGCTCAGTCTCCTGCGCATGCGC 425
QY 421 GGGGAGCGCTTGGCAGCAGTGTGGCGCGCGCGCGCGAGAGCGCGCGCGCGCACCAACACAGC 480
DB 426 ATTTAGCGCTTATTCACATGCTGAATAATGAACCTCCACAAACGGG---AGCAATTAACCTTC 482
QY 481 CGCGCTTACGCGCTTCATGCGCGCTGCTGCTGCTGCGCGCGCTGCTGCGGAGATGCTGCGCT 540
DB 483 CGCGCTTCTGCTTATGATCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542

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QY 541 TTGCTGGCTGGAAGTGGCTGTGCGCCCTTTTGACCGCTGCTCTACAGCTTTGCCCCCTTAC 600
DB 543 ATCATGGGCTGGAAGTGCATGATGAGCGCTGTCAAGCTGCTCCACCGTGCCTGCCCTCTAC 602
QY 601 TCCAGCGCTACATCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 603 CACAAGCATATATCTCTTGTGCAACACAGCGCTTTCACCTGCTGCTGCTGCTGCTGCTGCTGCT 662
QY 661 GCGCTCTATGAGGCGCATCTTCCGCTGCTGCAAGCCAGCGGCGGAGAGCGCCACGCCCA 720
DB 663 ATTTGACTGTCAGATATCTCTTGTGCTGCAAGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCT 722
QY 721 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 759
DB 723 AAGAACATTTCCAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTA 782
QY 760 CTGATGATCTGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
DB 783 ATTTAGCTGCTGAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
QY 820 GACGCTTTGGCTCCAACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 879
DB 843 GATG---TGGGCTGCAAGGTGAAGACCTGTGACATCTTCAAGAGCGGTACTTCTCTG 899
QY 880 GCCCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
DB 900 GTTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
QY 940 GTGTGCAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
DB 960 ATGCGTGGCGCGCTTCAATCCGATCATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 994

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RESULT 15
US-09-971-228-1
; Sequence 1, Application US/09971228
; Patent No. US2002015512A1
; GENERAL INFORMATION:
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Esteban
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Jorge
; APPLICANT: Li, Congfen
; APPLICANT: Zhao, Haoran
; APPLICANT: Jiang, Yingping
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Edg: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310US
; CURRENT APPLICATION NUMBER: US/09/971,228
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/284,763
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: wild-type human endothelial differentiation
; OTHER INFORMATION: G-protein coupled receptor (GPCR) 1 (EDG1)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION: wild type human EDG1
US-09-971-228-1

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Query Match      20.6%; Score 237.4; DB 9; Length 1149;
Best Local Similarity 55.7%; Pred. No. 4.8e-36;
Matches 554; Conservative 0; Mismatches 411; Indels 30; Gaps 4;

QY 1 ATGAAGCCACGGGAGACCCCGGTGGCCCGAGTCTGCAACACAGTGGCGCGCGG 60
DB 1 ATGAAGCCACGGGAGACCCCGGTGGCCCGAGTCTGCAACACAGTGGCGCGCGG 60

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 08:33:56 : Search time 2202 Seconds  
(without alignments)  
8494.908 Million cell updates/sec

Title: US-09-786-926-2  
Perfect score: 1155  
Sequence: 1 atgaacgcccacggagaccc.....ccagcgicgagagatctga 1155

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estlun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	874	75.7	907	9	AL560608
2	775	67.1	886	9	AL560216
3	763.2	66.1	804	13	BI910894
4	739.2	64.0	793	12	BG744043
5	692.6	60.0	930	13	BI824604
6	679.4	58.8	1057	14	BM922943

Result No.	Score	Query Match	Length	DB ID	Description
7	642	55.6	642	13	BI908610
8	636.8	55.1	790	12	BG685395
9	608.2	52.7	795	9	AL581703
10	606.8	52.5	707	9	AL543816
11	593.2	51.4	957	9	AL582021
12	560	48.5	1506	13	BM550147
13	551	47.7	998	10	BB610504
14	495	42.9	725	13	BI762628
15	458.4	39.7	687	12	AZ733984
16	391	33.9	729	17	BG744713
17	355.2	30.8	711	9	AL543781
18	339	29.4	348	13	BI909157
19	339	29.4	350	13	BI906532
20	339	29.4	1202	13	BM922670
21	321.6	27.8	352	13	BI908474
22	317	27.4	347	13	BI905951
23	317	27.4	352	13	BI834290
24	312.8	27.1	355	13	BI907722
25	309	26.8	783	13	BI906435
26	294	25.5	294	13	BI907726
27	289.8	25.1	359	13	BI909499
28	280.2	24.3	630	9	AL158682
29	278.8	24.1	422	9	AA51451
30	273.2	23.7	506	13	BM153127
31	268	23.2	390	12	BF901012
32	261	22.6	1731	14	BM918965
33	248.8	21.5	467	9	AL158066
34	242.6	21.0	578	13	BM483023
35	235	20.3	635	14	BQ053747
36	223.4	19.3	511	9	AL463732
37	221.6	19.2	3015	11	AK004591
38	214.4	18.6	237	12	BF916992
39	211.4	18.3	426	9	AA254425
40	208.6	18.1	354	13	BI907186
41	205.6	17.8	973	13	BI839010
42	203.4	17.6	745	12	BF281109
43	200.4	17.4	603	12	BF663028
44	200.4	17.4	603	12	BG397972
45	200.4	17.4	609	12	BF974516

## ALIGNMENTS

RESULT 1  
LOCUS AL560608 907 bp mRNA linear EST 16-FEB-2001  
DEFINITION LTI\_NFL010\_BC2 Homo sapiens cDNA clone CS0DL003YC21 5  
ACCESSION AL560608  
VERSION AL560608  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 907)  
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

## FEATURES

Location/Qualifiers  
1..907  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DL003YC21"  
/clone\_11b="LTI\_NFL010\_BC2"  
/sex="male"  
/tissue="male"  
/note="Vector: pcMVSPORT 6, Site\_1: NotI, 1st strand cDNA"

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9600 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : filiang@lifetech.com URL :  
<http://fulllength.invitrogen.com>

BASE COUNT 105 a 327 c 299 g 176 t  
 ORIGIN

Query Match 75.7% Score 874; DB 9; Length 907;  
 Best Local Similarity 99.7% Pred. No. 1.7e-144;

Matches 907; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 15 GACCCGGTGGCCCCGAGTCTGCGACACAGCTGGCGCGCGGCGACACGCCGCTCAT 74  
 DB 1 GACCCGGTGGCCCCGAGTCTGCGACACAGCTGGCGCGCGGCGACACGCCGCTCAT 60  
 QY 75 TTTTCTGCACTACACACACTCGGGCGGCTGGCGCGCGGCGCGGCGGAGGATGGCGG 134  
 DB 61 TTTTCTGCACTACACACACTCGGGCGGCTGGCGCGCGGCGCGGAGGATGGCGG 119  
 QY 135 CTTGGGGGCTGGGGGGGCTGTCGGTGGCGCGCGGCGGCGGCGGAGGATGGCGG 194  
 DB 120 CTTGGGGGCTGGGGGGGCTGTCGGTGGCGCGCGGCGGCGGAGGATGGCGG 179  
 QY 195 GCTGGTGGCGGCGATCACACAGCAGTGGCGGAGGCGGCTGCTACTATTGGCT 254  
 DB 180 GCTGGTGGCGGCGATCACACAGCAGTGGCGGAGGCGGCTGCTACTATTGGCT 239  
 QY 255 GGTGAACATCAGCTGAGTACCTGCTCAACGCGGCGGCGGCTACTGCGCAAGTGGTGT 314  
 DB 240 GGTGAACATCAGCTGAGTACCTGCTCAACGCGGCGGCGGCTACTGCGCAAGTGGTGT 299  
 QY 315 GTGGGGGGCGGCGACCTTCGCTGTCGGCGCGGCGGCGGCGGAGGAGGCGCTGCT 374  
 DB 300 GTGGGGGGCGGCGACCTTCGCTGTCGGCGCGGCGGCGGCGGAGGAGGCGCTGCT 359  
 QY 375 GTTCAACGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434  
 DB 360 GTTCAACGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419  
 QY 435 CACCATGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 494  
 DB 420 CACCATGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 479  
 QY 495 CATGGGCTGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 554  
 DB 480 CATGGGCTGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539  
 QY 555 GTGCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 614  
 DB 540 GTGCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599  
 QY 615 CTTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 674  
 DB 600 CTTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 659  
 QY 675 CATCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 734  
 DB 660 CATCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 718  
 QY 735 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 794  
 DB 719 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 778  
 QY 795 CCGACTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 854  
 DB 779 CCGACTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 838  
 QY 855 CTTGGGGGGCGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914

DB 839 CCTGGGGGCGATGAGTCTGAGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 897  
 QY 915 CATCTACTCC 924  
 DB 898 CATCTACTCC 907

# RESULT 2

AL560216 886 bp mRNA linear EST 16-FEB-2001  
 LOCUS AL560216 LTI\_Fl011\_Bc1 Homo sapiens cDNA clone CS00G002YR22 5 prime  
 DEFINITION / mRNA sequence.

ACCESSION AL560216  
 VERSION AL560216.1 GI:12906465  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 886)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

# FEATURES

source  
 1. 886  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="LTI\_Fl011\_Bc1"  
 /sex="male"  
 /issue\_type="R cells from Burkitt lymphoma"  
 /lab\_host="DH10B"  
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9600 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL :  
<http://fulllength.invitrogen.com>

BASE COUNT 103 a 311 c 299 g 172 t 1 others  
 ORIGIN

Query Match 67.1% Score 775; DB 9; Length 886;  
 Best Local Similarity 98.9% Pred. No. 4.7e-127;  
 Matches 809; Conservative 0; Mismatches 5; Indels 4; Gaps 3;

QY 1 ATGAACGCGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60  
 DB 2 ATGAACGCGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 61  
 QY 61 CACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
 DB 62 CACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 121  
 QY 121 CCGAGAGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 DB 122 CCGAGAGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 181  
 QY 181 GTGCTGAGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 DB 182 GTGCTGAGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241  
 QY 241 GTCTACTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
 DB 242 GTCTACTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301



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301 GCCAAGCTGCTGCTGTCGAGGAGCCCGACACTTCGCTGAGGCGCCCGCCAGTGTCTCTA 360
302 GCCAAGCTGCTGCTGTCGAGGAGCCCGACACTTCGCTGAGGCGCCCGCCAGTGTCTCTA 361
361 CGGAGAGGCTGCTGCTGTCACCGCCCGCCCTCCACCTTCACGCTGCTCTTCACTGCA 420
362 CGGAGAGGCTGCTGCTTCAACCGCCCGCCCTCCACCTTCACGCTGCTCTTCACTGCA 421
421 GGGGAGGCTGTCACCACTGCTGAGGCGCCGTGCGCCAGAGCGGGGCCACCAAGACCAG 480
422 GGGGAGGCTGTCACCACTGCTGAGGCGCCGTGCGCCAGAGCGGGGCCACCAAGACCAG 481
481 CGGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
482 CGGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
541 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
542 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
601 TCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
602 TCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
661 GGGCTTATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
662 GGGCTTATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
721 GGGCGCCGCGGACGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
722 GGGCGCCGCGGACGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
781 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
779 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815

RESULT 3
BI910894/c 804 bp mRNA linear EST 16-OCT-2001
LOCUS 603067667F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:521633 5',
DEFINITION mRNA sequence.
ACCESSION BI910894
VERSION BI910894.1 GI:16174354
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 804)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgrabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: MGC Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM1544 row: e column: 18
High quality sequence stop: 802.
Location/Qualifiers
1..804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:521633"
/clone_1ib="NIH_MGC_118"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; site_1: NotI; Site_2: EcoRV

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(destroyed): RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
BASE COUNT 159 a 254 c 297 g 94 t
ORIGIN

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Query Match 66.1%; Score 763.2; DB 13; Length 804;
Best Local Similarity 99.1%; Pred. No. 5,66-125;
Matches 799; Conservative 0; Mismatches 3; Indels 4; Gaps 3;

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255 GGTGAACATCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 313
804 GGTGAACATCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 745
314 TGTGGGGGGCCCGACCTTCCGCTGAGCG -CCGCGCCAGTGTCTTCAAGGAGGCTTG 372
744 TGTGGGGGGCCCGACCTTCCGCTGAGCG -CCGCGCCAGTGTCTTCAAGGAGGCTTG 685
373 CTCTTACAGCGCCGCGCGCTTCCACCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
684 CTCTTACAGCGCGCTTCCAGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625
433 GGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 492
624 GGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
493 TTCAATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
564 TTCAATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 505
553 AACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
504 AACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445
613 ATTCCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
444 ATTCCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 385
673 GCCATCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
384 GCCATCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325
733 AAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
324 AAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265
793 GGGCCACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 852
264 GGGCCACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 205
853 TACCTGCGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
204 TACCTGCGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 147
913 ATCATCTACTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
146 ATCATCTACTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 87
973 GGGGTCTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
86 GGGGTCTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27
1033 CACTTCGGAGCTTCCACACCGACAG 1058
26 CACTTCGGAGCTTCCACACCGACAG 1

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RESULT 4

BG744043 793 bp mRNA linear EST 15-MAY-2001  
 LOCUS 602722823F1 NIH\_MGC\_106 Homo sapiens cDNA clone IMAGE:4849349 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG744043  
 VERSION BG744043.1 GI:14054696  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 793)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Dr. Daniel McVicar, DBS/MCI  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: LHCMI688 row: n column: 06  
 High quality sequence stop: 783.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4849349"  
 /clone\_1lb="NIH\_MGC\_106"  
 /tissue\_type="natural killer cells, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: blood; Vector: pGB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."  
 BASE COUNT 95 a 284 c 270 g 144 t  
 ORIGIN  
 Query Match 64.0%; Score 739.2; DB 12; Length 793;  
 Best Local Similarity 99.2%; Pred. No. 9.5e-121;  
 Matches 764; Conservative 0; Mismatches 3; Indels 3; Gaps 2;  
 QY 1 ATGAAGCGACGAGCGGACCCCGGTGGCCCGAGTCCGACACAGCTGGCGGCGGCGG 60  
 |||||||  
 DB 27 ATGACGCCACGCGGAGACCCCGGTGGCCCGAGTCCGACACAGCTGGCGGCGGCGG 86  
 |||||||  
 QY 61 CACAGCGGCTCATTTGTTCTGCACTACACACACTCGGGCCGCTGGCGGCGGCGG 120  
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 DB 87 CACAGCGGCTCATTTGTTCTGCACTACACACACTCGGGCCGCTGGCGGCGGCGG 146  
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 QY 121 CCGGAGAGTGGCGGCTGGGGCCCTGGGGGGCTGCTGCTGGCGGCCCGACGCTGGTG 180  
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 DB 147 CCGGAGAGTGGCGGCTGGGGCCCTGGGGGGCTGCTGCTGGCGGCCCGACGCTGGTG 206  
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 QY 181 GTGCTGGAGAACTTCTGCTGGTGGCGGCATACACAGCCACATGCGGTGGCGAGCTGG 240  
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 DB 207 GTGCTGGAGAACTTCTGCTGGTGGCGGCATACACAGCCACATGCGGTGGCGAGCTGG 266  
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 QY 241 GTCTACTATGCTGCTGTAACATCAGCTGAGTACCTGCTACGGGCGGCGGCTACTAC 300  
 |||||||  
 DB 267 GTCTACTATGCTGCTGTAACATCAGCTGAGTACCTGCTACGGGCGGCGGCTACTAC 326  
 |||||||  
 QY 301 GCCAACGTGCTGCTGCGGGGGCGGACGCTGCTGCTGGCGGCCCGGACGTGGTTCTCA 360  
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 DB 327 GCCAACGTGCTGCTGCGGGGGCGGACGCTGCTGCTGGCGGCCCGGACGTGGTTCTCA 386

QY 361 CGGAGAGGCGCTGCTCTTACACGCGCCCTGGCCGCTCCACCTTACGCTCTTACAGCA 420  
 |||||||  
 DB 387 CGGAGAGGCGCTGCTCTTACACGCGCCCTGGCCGCTCCACCTTACGCTCTTACAGCA 446  
 |||||||  
 QY 421 GGGAGAGGCGCTTGGACACATGAGTGGCGGCTGGCGGAGAGGAGGAGGAGGAGGAGGAGG 480  
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 DB 447 GGGAGAGGCGCTTGGACACATGAGTGGCGGCTGGCGGAGAGGAGGAGGAGGAGGAGGAGG 506  
 |||||||  
 QY 481 CGGCTCTACGCGCTTCATCGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 |||||||  
 DB 507 CGGCTCTACGCGCTTCATCGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566  
 |||||||  
 QY 541 TTGCTGGGCTGGAACTGCGCTGGCGCTTGGACGCGTGGCGGACGCGCTTGGCGCTTAC 600  
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 DB 567 TTGCTGGGCTGGAACTGCGCTGGCGCTTGGACGCGTGGCGGACGCGCTTGGCGCTTAC 626  
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 QY 601 TCCAAAGCGCTACATCTCTTCTGCTGCTGATCTTGGCGGCGCTCTGGCCACATCATG 660  
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 DB 627 TCCAAAGCGCTACATCTCTTCTGCTGCTGATCTTGGCGGCGCTCTGGCCACATCATG 686  
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 QY 661 GGCTCTATGGGGCCATCTTCGGCTGTGTCAGGCGAGCGGCGAGAGGCGCCACAGCCCA 720  
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 DB 687 GGCTCTATGGGGCCATCTTCGGCTGTGTCAGGCGAGCGGCGAGAGGCGCCACAGCCCA 746  
 |||||||  
 QY 721 GCGGCGCGCGCGGACGCGCGCGCTGCTGTAAGACGCTGCTGATATCTT 770  
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 DB 747 GCGG-CGCGGCGAAGGCGCGC--GCTGCTGAAGACGCTGATGATCTT 793

RESULT 5  
 B1824604 930 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603033534F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5174720 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1824604  
 VERSION B1824604.1 GI:15936154  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 930)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: LHAM11435 row: c column: 09  
 High quality sequence stop: 773.  
 Location/Qualifiers  
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 /clone\_1lb="NIH\_MGC\_115"  
 /lab\_host="DH10B"  
 /note="Organ: pooled brain, lung, testis; Vector:  
 pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."

BASE COUNT	134 a	308 c	297 g	191 t	
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Query Match	60.0%; Score 692.6; DB 13; Length 930;				
Best Local Similarity	93.0%; Pred. No. 1.6e-112;				
Matches 814; Conservative	0; Mismatches 49; Indels 12; Gaps 8;				
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DB	1 TACACACATCGGGCCGGGCGGCGGCGGGGGGGCCGGAGATGGCGCTCGGGGGCC				60
OY	145 CTGGGGGGGGTGTGTGGGTGGCCAGCTGCTGGTGGTGTGTGTGTGTGTGTGTGT				204
DB	61 CTGGGGGGGGTGTGTGGGTGGCCAGCTGCTGGTGGTGTGTGTGTGTGTGTGTGT				120
OY	205 GCGGCCATCACACGCCACATGCGGTGGCCAGCGTGGGTCTACTATTGCGTGGGAATC				264
DB	121 GCGGCCATCACACGCCACATGCGGTGGCCAGCGTGGGTCTACTATTGCGTGGGAATC				180
OY	265 ACGGTAGTGCATGCTACAGGGGGGGCGGCTTACTGTGGCAACGTGCTGTGTGTGTGT				324
DB	181 ACGGTAGTGCATGCTACAGGGGGGGCGGCTTACTGTGGCAACGTGCTGTGTGTGT				240
OY	325 GCGACCTTCGCTGTGGGGCC - GCCAGTGGTCTTACAGGAGGGCGCTCTTACCGC				383
DB	241 GCGACCTTCGCTGTGGGGCCCTTGGCCAGTGGTCTTACAGGAGGGCGCTCTTACCGC				300
OY	384 CCTGGCGCCCTTCACATTTACACCTGCTTACGTACGTGAGGGGAGCGCTTGCACATGGT				443
DB	301 CCTGGCGCCCTTCACATTTACACCTGCTTACGTACGTGAGGGGAGCGCTTGCACATGGT				360
OY	444 GCGGCGGTGGCCGAGAGCGGGGGCCACCACAGACAGCGCGGTCTACGCGTTATCGGCT				503
DB	361 GCGGCGGTGGCCGAGAGCGGGGGCCACCACAGACAGCGCGGTCTACGCGTTATCGGCT				420
OY	504 CTGCGGCTGCTGGCGCGGCTGTGTGGGATGTCTGCTTTGTGTGGGTGGAAATCGCTGTG				563
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OY	624 CCTGTGATCTTGGCGGCGTCTGGCCACCATCATGAGGCTCTATGGGGCATCTTCCG				683
DB	541 CCGTGATCTTGGCGGCGTCTGGCCACCATCATGAGGCTCTATGGGGCATCTTCCG				600
OY	684 CCGTGAGCGGCGACGGG - - - CAGAAAGGCCCAAGCCAGCGCGCGCCAGAGGCGG				740
DB	601 CCGTGAGCGGCGAGCTGGGCGAATGGCCCATCTGCCAGCGCGCGCCAGAGGCGG				660
OY	741 CGCGCTGAGAGAGGTGTGTGATGATCTGCTGGCTTCTTGTTGTGT - GGGGCCAC				799
DB	661 CTG - CTGCTGAAAGAGGTGTGTGATGATCTGCTGTGTGTGTGTGTGTGTGTGTGT				719
OY	800 TCTTGGCGGCTGCTGTGGCCGACGCTTGTGGTCCAACTCTGGGCCCAAGAGTACCGC				859
DB	720 TCTTGCAGGTGTGTGTGGCCGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT				777
OY	860 GGGGCGATGAGCTG - - ATCTTGGCCCTGGCCCTTCT - AACTCGGGGTCAACCCATCA				916
DB	778 GGGGCGATGAGCTGATTTTGTGGCCCTGGCAAGTCTCAAAATGAGCGGTAACACCATCA				837
OY	917 TCTACTCTTC - GCACGAGGAGGTGTGTCAAGC				950
DB	838 ACTATACTTCCAGCAGCGACGAGGTGTGTCAAAAC				872
RESULT 6					
LOCUS	BM922943	1057 bp	mRNA	linear	EST 12-MAR-2002
DEFINITION	A5ENSCOUTF_6632184 NIH_MGC_1118 Homo sapiens cDNA clone IMAGE:5756876				
	5', mRNA sequence.				

Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
B0922943	BM922943.1	GI:19373322	EST.	human.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	NIH-MGC http://mgi.nci.nih.gov/	1 (bases 1 to 1057)	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LHAM2798 Row: C Column: 21 High quality sequence stopper: 581.
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/clone_1ib="NIH_MGC_118"									
/tissue_type="Leukocyte"									
/lab_host="DH10B"									
/note="vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source: Leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is inserted upon cloning). Average insert size 1.7 kb. Insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: This is a NIH_MGC Library."									
BASE COUNT	118 a 418 c 333 g 188 t								
ORIGIN									
Query Match	58.8%; Score 679.4; DB 14; Length 1057;								
Best Local Similarity	91.0%; Pred. No. 3.5e-110;								
Matches 793; Conservative	0; Mismatches 61; Indels 17; Gaps 6;								
QY	1 ATGACGCCACGGGGAACCCCGGTGGCCCCAGTCTGCCAACAGTCGGCGCGGGCGGG 60								
DB	21 ATGAAACGCCACGGGGAACCCCGGTGGCCCCAGTCTGCCAACAGTCGGCGCGGGCGGG 80								
QY	61 CAAGCGCGGTCTATTGTTCGCACTACAACCAATCGGCGCGGTGGCGCGGGCGGGCGGG 120								
DB	81 CACAGCGGGGTCTATTGTTCGCACTACAACCACTCGGGCGCGGTGGCGCGGGCGGGCGGG 140								
QY	121 CCGGAGGATGGCGCCTGGGGGCGCTGGGGGGCGTGGTGCGCCGACGTGCTTGCTG 180								
DB	141 CCGGAGGATGGCGCCTGGGGGCGCTGGGGGGCGTGGTGCGCCGACGTGCTTGCTG 200								
QY	181 GTGCTGGAAGAATTGCTGGTGGTGGGGGGCATACACAGCACATGCGGTGGCGACCTGG 240								
DB	201 GTGCTGGAAGAATTGCTGGTGGTGGGGGGCATACACAGCACATGCGGTGGCGACCTGG 260								
QY	241 GTGTACTATTGCTGTGTAACATACAGCTGATGACCTGCTCAACGGGGCGGCGCTTACTG 300								
DB	261 GTGTACTATTGCTGTGTAACATACAGCTGATGACCTGCTCAACGGGGCGGCGCTTACTG 320								
QY	301 GCCAAGTGTGCTGTGGGGGGCGGACCTTCGTTGGCGCGCCGACAGTGGTTCTCTA 360								
DB	321 GCCAAGTGTGCTGTGGGGGGCGGACCTTCGTTGGCGCGCCGACAGTGGTTCTCTA 380								
QY	361 CGGAGAGGCTGTCTTACCAGCCCTGGCGGCTTCACACTTCAAGCTGCTTCTACTGCA 420								
DB	381 CGGAGAGGCTGTCTTACCAGCCCTGGCGGCTTCACACTTCAAGCTGCTTCTACTGCA 440								

Oy	421	GGAGAGCGCTTTGACCAACAGTGTGGGCGGGGCGCAGAGACGGGGGCACCAGAACACAG	480
Db	441	GGGAGCGCTTTGCCACCAATGGTGCGGCCGGTGGCCAGAGCGGGGCACCAAGACACAG	500
Oy	481	CAGCTACAGCGCTTACATCGGCGCTCTGTGAGCTGTGGCGCGCTGTGGAGATGTGCT	540
Db	501	CGCTTACAGCGCTTACATCGGCGCTCTGTGAGCTGTGGCGCGCTGTGGAGATGTGCT	560
Oy	541	TTCGTGGCGCTGAACAGCTGTGGCGCTTTTACACCGCTGTCCACACTTGTCCCGCTAC	600
Db	561	TTCGTGGCGCTGAACAGCTGTGGCGCTTTTACACCGCTGTCCACACTTGTCCCGCTAC	620
Oy	601	TCCAAGCGCTACATCTCTTTCGCCGTGGATCTTTCGCCGCGCTGTGGCCACCATATG	660
Db	621	TCCAAGCGCTACATCTCTTTCGCCGTGGATCTTTCGCCGCGCTGTGGCCACCATATG	680
Oy	661	GCGCTCAT-----GGGGGCATCTTCCGCTGTGTGACAGCCAG--CGGGAGAAGGGCCCCA	714
Db	681	GCGCTCATATGAGGGGGGGGGCTTTCGCCGTGTGTGACAGCCAGCCGCGCAAAGGGCCCCA	740
Oy	715	CGCCACAGCGCGCGCGCGCGCAA--GGCGCGCGCGCTGTGAGAGAGCGTGTCTG-ATGATCT	770
Db	741	CGCCCGCGCGCGCGCGCGCGCAAAGGGCGCGCGCGCTGTGAGAGAGCGTGTGATGACCT	800
Oy	771	GCTGGCTT---CCTGTGTGCTGTGGGGCGCCACTCTTGGGC---TCTCTGTGGCGAGC	823
Db	801	GCGCGCGCTTCCCGGGGGCGGTGGGGGGCCACACCTTCCGGGCTGTGTCCGTGGCCAGGC	860
Oy	~ 824	TCATTGCTCCAACTCTGTGGGCCAGAGTA	854
Db	861	CTTTGGGCGCCACACTCTGTGGGGCGCGGGAAA	891
RESULT 7	B1908610/c	B1908610	642 bp -mRNA linear EST 16-OCT-2001
LOCUS		603066721f1 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5215948 5',	
DEFINITION		mRNA sequence.	
ACCESSION		B1908610	
VERSION		B1908610.1 GI:16171625	
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE		1 (bases 1 to 642)	
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/.	
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)	
		Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LHAM1542 row: 1 column: 05 High quality sequence stop: 641. Location/Qualifiers	
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		/clone="IMAGE:5215948"	
		/cdna_lib="NIH_MGC_118"	
		/tissue_type="Leukocyte"	
		/lab_host="DH10B"	
		/note="vector: pCMV-SPORT6, Site.1: NotI, Site.2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon	

cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH-MGC Library.

BASE COUNT	135 a	201 c	233 g	73 t
ORIGIN				
Query Match	55.6%	Score 642:	DB 13:	Length 642:
Best Local Similarity	100.0%	Pred. No. 1,2e-103:		
Matches	642:	Conservative	0:	Mismatches 0: Indels 0: Gaps 0:
OY	238	TTGGTCTACTATTATGCTGCTGTGAACATCAACGCTGATGACCTGCTCACAGGAGCGGCGCTTAC	297	
DB	642	TGGGTCTACTATTATGCTGCTGTGAACATCAACGCTGATGACCTGCTCACAGGAGCGGCGCTTAC	583	
OY	298	CTTGCCCAACCTGCTGCTGTCGCGGGGCGCCGACCTTCCGCTGGGCGCCCGCCAGTAGTGTTC	357	
DB	582	CTGCGCCAACTGCTGCTGTCGCGGGGCGCCGACCTTCCGCTGGGCGCCCGCCAGTAGTGTTC	523	
OY	358	CTACGGAGAGGCGCTGCTCTTTCACCGCGCCCGCTCCACCTTCACCTTCAGCTGCTCTTCACT	417	
DB	522	CTACGGAGAGGCGCTGCTCTTTCACCGCCCGCTCCACCTTCAGCTGCTCTTCACT	463	
OY	418	GCAGGAGAGCGCTTTCGCCACCATGCTGGGCGCGGTGGCGCCAGAGCGGAGCCACACAGACC	477	
DB	462	GCAGGAGAGCGCTTTCGCCACCATGCTGGGCGCGGTGGCGCCAGAGCGGAGCCACACAGACC	403	
OY	478	AGCGCGCTCTACGGCTTTCATCGGCGCTTGTGCTGCTGGCGCGCGCTGCTGGGAGTCTG	537	
DB	402	AGCGCGCTCTACGGCTTTCATCGGCGCTTGTGCTGCTGGCGCGCGCTGCTGGGAGTCTG	343	
OY	538	CGTTTGTGGGGCTGGAGCACTGCTGCGCCCTTTTACACGCTGCTCCAGCCTTGTGCGCCCTC	597	
DB	342	CGTTTGTGGGGCTGGAGCACTGCTGCGCCCTTTTGAACGCTGCTCCAGCCTTGTGCGCCCTC	283	
OY	598	TATCTCCAAAGCGCTACATCTCTTCTGCTGCTGATCTTCCGCGCGCTCTCGGCGACATAC	657	
DB	282	TATCTCCAAAGCGCTACATCTCTTCTGCTGCTGATCTTCCGCGCGCTCTCGGCGACATAC	223	
OY	658	ATGGGCTCTATATGGGGCCATCTTCCGCGCTGGTGCAGGCGCACAGCGGCGAGAAAGGCCCGACGC	717	
DB	222	ATGGGCTCTATATGGGGCCATCTTCCGCGCTGGTGCAGGCGCACAGCGGCGAGAAAGGCCCGACGC	163	
OY	718	CCACGGGCGCGCGCGCAAGGCGCGCGCGCGCTGGAAGAGCGGTGATGATCCGCTGGCGGC	777	
DB	162	CCACGGGCGCGCGCGCAAGGCGCGCGCGCTGGAAGAGCGGTGATGATCTGCTGGCGGC	103	
OY	778	TTTCTGTGTGTGCTGGGGGCCCACTCTTTCGGGCTGCTGTGCGCGCAGAGCTTTTGGCTCCAAAC	837	
DB	102	TTTCTGTGTGTGCTGGGGGCCCACTCTTTCGGGCTGCTGTGCGCGCAGAGCTTTTGGCTCCAAAC	43	
OY	838	CTCTGGGGCCGAGAGTACCTGGGGGGGCAAGGAGCTGAGATCCCG	879	
DB	42	CTCTGGGGCCGAGAGTACCTGGGGGGGCAAGGAGCTGAGATCTCG	1	
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LOCUS	602637082f1 NIH_MGC_48			
DEFINITION				
ACCESSION	B6685195			
VERSION	B6685195.1			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	NIH-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			



QY	Db	Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
529	CTGCTGGACCTTCTTGATGTCGTGGGGCCACACTTTCGGGGCTGCTGCTGGCCAGAGTCTTT	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
829	GGCTCCAACTCTGGGGCCAGAGATACCTGGGGGATGACTGGATCTGGCCCTGGCC	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
469	GGCTCCAACTCTGGGGCCAGAGATGTA-CTGGCGRACATGAGACTGATCTGGGGCTGGCC	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
889	GTCTTCACACTGGGGCTCAACCCCATCATCTACTCTCTCCAGACAGAGAGTGTGACA	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
410	GTCTTCACACTGGGGCTCAACCCCATCATCTACTCTCTCCAGACAGAGAGTGTGACA	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
949	GGCTGTCTACACTCTCTCTGCTGCGGGGTCTCTCGGGCTGGGATGCGAGGGCCGGGAC	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
350	GGCTGTCTACACTCTCTCTGCTGCGGGGTCTCTCGGGCTGGGATGCGAGGGCCGGGAC	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
1009	TGCTGTGGCCGGGGCTGCGAGGCTACTCCGAGGCTTCACACGACGACTCTTGAGG	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
290	TGCTGTGGCCGGGGCTGCGAGGCTACTCCGAGGCTTCACACGACGACTCTTGAGG	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
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230	CCAGGAGACAGCTTTCGGGGCTCCGGCTCCGAGGCTTCGAGAGCGGAGCCCGTGTCC	AL543816	1	EST	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
QY	1129	AGCATCTCCAGCGTGGGAGCATCTGA	1155								
Db	170	AGCATCTCCAGCGTGGGAGCATCTGA	144								
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AL543816											
LOCUS											
DEFINITION											
ACCESSION											
VERSION											
KEYWORDS											
SOURCE											
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AUTHORS											
TITLE											
JOURNAL											
COMMENT											
FEATURES											
source											
BASE COUNT											
ORIGIN											
Query Match											
Best Local Similarity											
Matches											
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Match	Conservative	90.7%	Pred. No. 2e-97								
Matches	641	Conservative	31	Mismatches	29	Indels	6	Gaps	3		

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Db      1 CTGCCAAMAGCTGGCGGCGCGGGGACAGCCGGCTCATTTGTTCGCATCACAACCACACTC 60
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Db      61 GGGCGGGCTGGCGGGGCGGGGGGCGCGKANKANTGCGGYTTGGGGCGCTCGCGGGGCT 120
OY      156 GTGCTGGCGCGGAGCGCTGGTGCTGGTGG---ACAACTTCCTGGTGGCGGCA 211
Db      121 TTGCGTGGCGCGTAATYTGGTGGTGGTGGTGGTGAATGAATMTGCTGGTTCGGGCCA 180
OY      212 TCAC-CAGCCACATGGGGTGGCGAGCGCTGGGTCTATTGCTCGGTGAACATCACGCTG 270
Db      181 TCACTCACAACATWCTKTCKGACACTTGGTCTACTATTCCGTMGAAMATCACACTG 240
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OY      331 TTCGCTTGGCGCGCGCCC-AGTGGTCTTACGGGAGGGCGCTGCTTTACCGCGCTGG 389
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OY      450 GGTGGCGGAAGGGGGGCGCACCAAGACAGCGCGCTTACAGGCTTACATGGCGCTTGG 509
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OY      510 GCTGCTGGCGCGCTGCTGAGGATGCTGGCTTGGTGGGCTGGAACCTGTCGCGCTT 569
Db      481 GCTGCTGGCGCGCGCTGCTGAGGATGCTGCTTGGTGGGCTGGAACCTGTCGCGCTT 540
OY      570 TGACCGCTGCTCAGAGCTTCTGGCCCTTCACTCAAGAGGCTACATCCTTTTGGCTGG 629
Db      541 TGACCGCTGCTCAGAGCTTCTGGCCCTTCACTCAAGAGGCTACATCCTTTTGGCTGG 600
OY      630 GATCTTGGCGCGGCTCTTGCGCACCATATGAGGCTCTATGGGGCCATCTTCCGCGCTGG 689
Db      601 GATCTTGGCGCGGCTCTTGCGCACCATATATRGCTCTATRGGGCCATCTTCCGCGCTGG 660
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RESULT 11
AL582021/c 957 bp mRNA linear EST 16-FEB-2001
LOCUS     AL582021 LRT.NFL010.BC2 Homo sapiens cDNA clone CSDDL003YC21 3
DEFINITION prime, mRNA sequence.
ACCESSION AL582021
VERSION   AL582021.1 GI:12949597
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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Db	421	GGGGCCACCAAGACACAGCCCGGCTCAGCGCTTCATCGCCCTTCGTGTGGCTGCTGCTGCGCGG	480	
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Db	481	CTGCTGGAGATGCTGCGCTTTGCTGGGCTGGAAAGTCCGTGCGCTTTGACCGCTGCTC	540	
QY	582	CAGCTTTCCTCCCTCTACTCCCAAGG-CCTACATCTCTCTCTG-CCTGCGATCTTGGCC	639	
Db	541	CAACCTTCTGCGCCCTCTACTCCCAAGCGCCTACATCTCTCTTCTGCGCGTGGGATCTTCC	600	
QY	640	GGCTCTCTGGCCACACATCAT	659	
Db	601	CGCGCTCTCTGGCGCACCAT	620	
RESULT 13				
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LOCUS			linear	
DEFINITION	BB610504	RIKEN full-length enriched, adult male stomach	Mus	
ACCESSION	BB610504			
VERSION	BB610504.1	GI:16452020		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 998)			
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,E., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,H., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,I., Toya,T., Muramatsu,M. and Hayashizaki,Y.			
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenro-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resgsc.riken.go.jp, url:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuhiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamane,K., I., Aizawa,M., K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. Location/Qualifiers 1..998			

[illegible]







GenCore version 5.1.3  
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## OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 08:37:36 ; Search time 75 Seconds

(without alignments)  
4722.822 Million cell updates/sec

Title: US-09-786-926-2

Perfect score: 1155

Sequence: 1 atgaagccacagggagacc.....ccagcgtcgagacatcga 1155

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Database : Issued Patents NA:\*

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- 2: /cgn2\_6/prodata/1/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/PCTUS.COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1142.2	98.9	1637	3	US-08-852-824-3
2	1104.8	95.7	1639	2	US-08-845-566-2
3	254.4	22.0	1137	4	US-09-082-088-1
4	254.4	22.0	1137	4	US-09-546-117-1
5	237.4	20.6	1149	4	US-09-262-477-1
6	230.2	19.9	2232	1	US-08-196-989B-3
7	230.2	19.9	2232	1	US-08-760-936-3
8	221.6	19.2	1149	4	US-09-542-733-1
9	182	15.8	1260	3	US-08-789-982-1
10	178.8	15.5	1761	3	US-08-861-747-1
11	168.4	14.7	2754	1	US-08-861-747-3
12	168.4	14.7	2754	1	US-08-196-989B-1
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14	129.4	11.2	2250	3	US-08-763-938-1
15	114	9.9	2185	2	US-08-467-948A-3
16	114	9.9	2185	3	US-08-467-947A-3
17	113.2	9.8	1065	4	US-09-325-897-1
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20	111.8	9.7	2126	2	US-09-110-937-1
21	111.8	9.7	2126	3	US-09-058-725B-1
22	111.8	9.7	2126	3	US-09-232-857-1
23	111	9.6	1356	3	US-08-997-803-13
24	111	9.6	1523	3	US-08-997-803-12
25	100.4	8.7	1089	4	US-09-513-838-1
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34	77.2	6.7	2140	1	US-08-334-698-1	Sequence 1, Appl1
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45	76.8	6.6	1370	1	US-07-928-611-17	Sequence 17, Appl1

## ALIGNMENTS

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RESULT 1
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; Sequence 3, Application US/08852824C
; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.1220000
; CURRENT APPLICATION NUMBER: US/08/852.824C
; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1637
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1201)
US-08-852-824-3
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QY	61	CACAGCCGCTCATTTGCTGCTGACACTAACCACTCGGCGGCTGGCGGCGGCGGCGG	120			
DB	110	CACAGCCGCTCATTTGCTGCTGACACTAACCACTCGGCGGCTGGCGGCGGCGGCGG	169			
QY	121	CCGAGGATGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	180			
DB	170	CCGAGGATGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	229			
QY	181	GTCGTGGAACATCTGCTGCTGCTGCGGCATCACAGCCATGCGTGGCGAGCGCTGG	240			
DB	230	GTCGTGGAACATCTGCTGCTGCTGCGGCATCACAGCCATGCGTGGCGAGCGCTGG	289			
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QY	361	CGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420			

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Db 470 GGGTTGCGCTTGGCCACATGTCGGGCGGTCGCGGAGAGCGGAGGCGCCACCAAGACACG 529  
QY 481 CGGCTTACGAGCTTACGAGGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 540  
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Db 590 TTGCTGAGCTGGAACCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 649  
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QY 721 GGGGCGCGCGCGAGGCGCGCGCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 780  
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RESULT 2  
US-08-845-566-2  
; Sequence 2, Application US/0845566  
; Patent No. 5912144  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Guegler, Karl  
; TITLE OF INVENTION: EDG-1 LIKE RECEPTOR  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:

Query Match 95.7% Score 1104.8; DB 2: Length 1649;  
Best Local Similarity 99.2%; Pred. No. 1.5e-199;  
Matches 1150; Conservative 0; Mismatches 5; Indels 4; Gaps 4;  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845.566  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0271 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1649 base pairs  
TYPE: nucleic acid  
STRADEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: TYNMOR01  
CLONE: 144690  
US-08-845-566-2

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 QY 1018 GCGGCGCTGAGAGCTACCTCCGAGAGCTTC -ACGACGAGAGCTGCTGAGCGCAAGGA 1076  
 DB 1030 GCGGCGCTGAGAGCTACCTCCGAGAGCTTCACGAGAGCTGCTGAGCGCAAGGA 1089  
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 RESULT 3  
 US-09-082-088-1  
 ; Sequence 1, Application US/09082088  
 ; Patent No. 6130067  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSUI, PING  
 ; TITLE OF INVENTION: HUMAN EDG3sb GENE  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Ratner & Prestlia  
 ; STREET: P.O. Box 980  
 ; CITY: Valley Forge  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/082,088  
 ; FILING DATE: 20-MAY-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Prestlia, Paul F.  
 ; REGISTRATION NUMBER: 23,031  
 ; REFERENCE/DOCKET NUMBER: GP-70453  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1137 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 US-09-082-088-1  
 Query Match 22.0%; Score 254.4; DB 3; Length 1137;  
 Best Local Similarity 56.6%; Pred. No. 8.3e-40;  
 Matches 512; Conservative 0; Mismatches 386; Indels 6; Gaps 2;  
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601 TCCAGGCGCTTCAATCGGCGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCG 660
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RESULT 6  
 US-08-196-989B-3  
 ; Sequence 3, Application US/08196989B  
 ; Patent No. 5585476  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MacLennan, A. John  
 ; TITLE OF INVENTION: Molecular Cloning and Expression of  
 ; TITLE OF INVENTION: G-Protein Coupled Receptors  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESS: Saliwanichik & Saliwanichik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: FL  
 ; COUNTRY: US  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196, 989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 269..1420
US-08-196-989B-3

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Query Match 19.94; Score 230.2; DB 1; Length 2232;
Best Local Similarity 55.3%; Pred. No. 3, 1e-35;
Matches 548; Conservative 0; Mismatches 413; Indels 30; Gaps 4;

2 TGAAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
273 TGTCTCTCCAGCAGCATCCCATGCTGTAAGGCTCTCCGAGCCAGATCTCCATG 332
62 ACAAGCGCTCATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
333 ACTATGATATCATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 392
122 CGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
393 AGGAGCATGAGCATTAACGAGC---TTCAAGTGGTTCATTCATCTGCTGATGCA 449
182 TGTCTGAGAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
450 TCTTGAAGAAATATTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509
242 TCTACTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
510 TGTACTATTTCATAGGCAACCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 569
302 CCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
570 CTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629
362 GGGAGGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
630 GGGAGGAGAAATATTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
422 GGGAGGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
690 TTGAGCGCTTATCATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746
482 GCGCTTACGCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
747 GCTCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 806
542 TGTGAGGCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
807 TCATGAGGCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866
602 CCAAGCGCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661

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Db 867 ACAACACTATATCTCTCTGACACCGCTCTACCCCTGCTCTTCATGCTCA 926
QY 662 GCGCTATAGGGCCATCTTCCGCTGCTGACAGCGCCAGAGGCCCAAGCCCA 721
Db 927 TCCCTACTGAGAGATCTACTCTCTGAGAGCTGAGAGCGCGGCTGACCTTCCGA 986
QY 722 CGGCGCGCGAGAGCGCGCGG-----CCTGCTGAAGAGGTG 760
Db 987 AGAATCTCCAGAGCGCGAGCTTCCGAGAGTCTGCGCTTCTGTGAAGCAGTGA 1046
QY 761 TGAATATCTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
Db 1047 TCAATGCTCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
QY 821 ACGTCTTGCTCCACCTCTGCGCGCAGAGTACCTGCGGCGAGTGAAGTCTGCTG 880
Db 1107 ATG---TGGGTCGACAGGCGAGACCTGTGACATCTCTTACAAAGAGAGTCTG 1163
QY 881 CCGTGGCGCTCTCACTCGGCGCTCAACCCATCATCTCTCTCCGACAGAGGAG 940
Db 1164 TTTGCTGCTGCTCACTCACTGAGTACCAACCCATCATCTCTGACCAATAGGAGA 1223
QY 941 TGTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
Db 1224 TCGCGCGGCGCTTCAATCAGATCATATCTTG 1254

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## RESULT 7

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US-08-760-936-3
; Sequence 3, Application US/08760936
; Patent No. 5856443
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; -TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,936
; FILING DATE: December 6, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Page, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 269..1420
; US-08-760-936-3

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Query Match 19.9%; Score 230.2; DB 2; Length 2232;  
 Best local, similarity 55.3%; Pred. No. 3, 1e-35;

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Matches 548; Conservative 0; Mismatches 413; Indels 30; Gaps 4;
QY 2 TGAACGCCAGGGAGACCCGCGGCGCCCGAGTCTGCCAAGCTGAGCGCGCGG 61
Db 273 TGTCTCCACAGGATCCAGTGTAAAGCTCTCCAGGCAAGTCTCCGATATGGA 332
QY 62 ACAGCGGCTATGTTCTGACACACACTCGGCGCGGCTGAGCGCGGCGCGG 121
Db 333 ACTATGATATATATAGTCCGGCATTAACACTACAGAGCAAGCTGACATGAGTGA 392
QY 122 CGAGAGATGCGCGCTGCGGCGCTCGGCGGCTGCGAGCGCGAGCTGCTG 181
Db 393 AGACCATATATATTAACCTGAC---TTCAGTGTGTATCTATCTGCTGTGATCA 449
QY 182 TCTGTGAGAACTTCTGCTGCTGCTGCGGACCATACAGCACATGCGGTCGAGAG 241
Db 450 TCTTGAAGATATATTTTCTGTGTAATTTTGGAAAAACCAAGATTCACCGGCCA 509
QY 242 TCTACTATTTGCTGTGTAACATACGCTGATGACCTGCTACGCGCGGCTTACTG 301
Db 510 TGTACTATTTTATAGGACACCTAGCCCTCGAGACCTGTAGCAGGAGTGGCTTAC 569
QY 302 CCAACGTCTCTGCTGCGGCGCGGACCTTCGCTGTGAGCGCGCGCAAGTGTCTAC 361
Db 570 CTAACTGCTCTGTGCTGCGGCGCACACCTACAGCTCAACACTGCGCAAGTGTCTG 629
QY 362 GGGAGGCGCTCTCTTACCGCGCGCTGCGCTCCACCTTACGCTGCTTACTGAC 421
Db 630 GGGAGGAGATATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 689
QY 422 GGGAGCGCTTGTCCACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 481
Db 690 TTGACGCTTACATCACCATGCTGTGAGATGAACCTACACAGG---CAGCAACGCT 746
QY 482 GCGTACGCGCTTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
Db 747 GCTCTTCTGCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 806
QY 542 TCGTGGGCTGAGATGCTGTGCGCTTGTGACCGCTGTGACAGCTTCTGCGCTTACT 601
Db 807 TCAATGGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 866
QY 602 CCAAGCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
Db 867 ACAACACTATATCTCTCTGACACCGCTCTACCCCTGCTCTTCATGCTCA 926
QY 662 GCGCTATAGGGCCATCTTCCGCTGCTGACAGCGCCAGAGGCCCAAGCCCA 721
Db 927 TCCCTACTGAGAGATCTACTCTCTGAGAGCTGAGAGCGCGGCTGACCTTCCGA 986
QY 722 CGGCGCGCGAGAGCGCGCGG-----CCTGCTGAAGAGGTG 760
Db 987 AGAATCTCCAGAGCGCGAGCTTCCGAGAGTCTGCGCTTCTGTGAAGCAGTGA 1046
QY 761 TGAATATCTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
Db 1047 TCAATGCTCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
QY 821 ACGTCTTGCTCCACCTCTGCGCGCAGAGTACCTGCGGCGAGTGAAGTCTGCTG 880
Db 1107 ATG---TGGGTCGACAGGCGAGACCTGTGACATCTCTTACAAAGAGAGTCTG 1163
QY 881 CCGTGGCGCTCTCACTCGGCGCTCAACCCATCATCTCTCTCCGACAGAGGAG 940
Db 1164 TTTGCTGCTGCTCACTCACTGAGTACCAACCCATCATCTCTGACCAATAGGAGA 1223
QY 941 TGTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
Db 1224 TCGCGCGGCGCTTCAATCAGATCATATCTTG 1254

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RESULT 8  
 US-09-542-733-1



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; Sequence 1, Application US/09542733
; Patent No. 6323333
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: Mouse EDG1
; FILE REFERENCE: GP-70610
; CURRENT APPLICATION NUMBER: US/09/542,733
; EARLIER FILING DATE: 2000-04-04
; EARLIER APPLICATION NUMBER: 60/127,696
; EARLIER FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: MUS MUSCULUS
US-09-542-733-1
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Query Match          19.2%; Score 221.6; DB 4; Length 1149;
Best Local Similarity 54.7%; Pred. No. 1,2e-33;
Matches 543; Conservative 0; Mismatches 419; Indels 30; Gaps 4;
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OY 1 ATGAACGACGAGGAGGAGCCGGGTCGCCCGGAGTCCTGCGCAACAGCTGGGGCGCGGGGG 60
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Db 1 ATGGTCCACTAGCATGCAATCCCGAGGTAAAGCTCTCCGACAGCTGCTCTGACTATGG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 CACAGCGGCGCTATGTTGCTGACTACACACACTCGGGCGCGCTGGCGGGGGGG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AACATGATATCATAGTCGCGCATTAACAACAGAGCAAGTTGAAC---ATCGGGGGCG 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 CCGGAGGATGGGGGCGCTGGGGGCGCTGGGGGGGCTGGGGGCGGCGAGCTGGCTG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 GAGAGGACCATGCGCTTAACTGACTTCAGTGTGTTCACTTCATCTGCTGCTTCATC 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 GTGCTGAGAACTTGTGCTGTGCTGGCGGCATCACACAGCATGCGGTGCGACGCTG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 ATCCGTAGAGAAATATATTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 241 GTCTACTATTGCTGGTGACATCAAGCTGAGTGCAGTCTGAGGGGGGGGCTTACTCT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db - 238 ATGTAATTTTCATGAGCAACTAGCCCTTCGAGCTATTGAGAGGCTGGCTTACACA 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 301 GCCAACGTGCTGCTGCGGGGGCGGACCTTCCGCTGCGGGCGCGCCAGGTTGCTCA 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 GCTAACCTGCTGTGTCTGGGGCGACCACTTACAGCTCACACCTGCCAGTGGTTCTG 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 361 CCGGAGGCGCTGCTCTTCAACGCGCGCTGCGCTTCACTTCACTGCTTCTTCACTGCA 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 CCGGAGGAGAGATGTTTGTGCTCTCTCTGATCATGCTTCACTGCTTCTTCACTGCGC 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 421 GGGGAGCGCTTTCACACATGATGGGCGCGGTGGCCGAGAGCGGGGCCACCAAGACGAGC 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 ATTGAGCGCTACATCACATGCTGTAAGATGAATACACACAGGG---AGCAAGAGCTG 474
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 481 CCGGCTTACGCGCTTACGCGCTGCTGCGCTGCTGCGCTGCGCTGCGCTGCGCTGCGCT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 475 CCGTCTTCTGCTGATCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 541 TTGCTGGGCTGGAATGCTGCTGCTTTCGACGCTGCTTCACTGCTTTCGCTTAC 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 ATCATGGGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
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OY 601 TCGAAGGCTACATCTCTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 CACAGACATATATTTCTCTTCTGACACACCGCTTTCATCTGCTGCTGCTTTCATGCTG 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 661 GGCCTCTATGAGGCGCATCTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 ATCTCTACTGACGATCTACTCTTGTGTCAGAGACTCGAAGCCCGCGCTGACTTTCGCG 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 721 GCGGCCGCGCGCAAGGCGCGCGG-----CGTGTGAAGAGGCTG 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 715 AAGAACATCTCCAGGCGCATGCTGAGAGTCTCTGCGCTTGTGTAAGAGGCTG 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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OY 760 CTGATGATCTGCTGCGCTTCTGCTGCTGCTGCGGCCACACTTTCGGGCTGCTGCGCC 819
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Db 775 ATCATGCTCTGAGTGCTTCATGCTGCTGCGGCCCTCTCTTCATCTTACTGTTA 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 820 GACGCTTTGGCTCCCAACCTCTGGGCCAGAGTACCTGCGGGGAGTGAATGCTG 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 835 GATG---TGGGCTGCAAGGAGAGCTGTGACATCTGTACAAAGAGAGTACTTCTG 891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 880 GCCCTGGCGCTCTCAACTGCGGCTCAACCCCATCATCTACTCTTCCGACAGAGGAG 939
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 892 GTTCTGCTGTGCTGAGACTGAGTACCAACCCCATCATCTACTCACTGACCAAGAGAG 951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 940 GTGTGACAGCCGTGCTCACTCTCTGCTG 971
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 952 ATGCGCGGCGCTTTCATCCGATCATCTTCTG 983
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RESULT 9
US-08-789-982-1
; Sequence 1, Application US/08789982
; Patent No. 6037146
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; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Bergsma, Dirk
; TITLE OF INVENTION: CDNA CLONE HEBC90 THAT ENCODES
; TITLE OF INVENTION: A NOVEL 7- TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,982
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-789-982-1
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Query Match          15.8%; Score 182; DB 3; Length 1260;
Best Local Similarity 53.8%; Pred. No. 3.3e-26;
Matches 477; Conservative 0; Mismatches 385; Indels 24; Gaps 4;
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OY 139 GGGGCGCTGCGGGGAGTGTGCTGCGCGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 229 GTGCTCGTGTGCGACATGCGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 199 GTGCTGGGCGCATCACAGCACATGCGGTGCGGACGCTGCGTCTACTATTGCTGCTG 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 289 GTCATACAGCATCGCTCCAAACCGCGCTTCACACAGCCCATCTACTACCTGGCGGC 348
Qy 259 AACATCAGCGGAGTGAACCTGCTACAGCGGCGCGCTTACTGGCCACAGCTGCTGTCG 318
Db 349 AATGTGCGCGGGGTGACCTCTTGCGGGGCTGACCTCTTCTCTCATGTTTCCACACT 408
Qy 319 GGGGCGCGGACCTTCGCTGCGGCGCCGACAGTGGTTCTTACAGGGAGCGCTGCTTCG 378
Db 409 GGTCCCGGACAGCCGACTTTCATTTAGAGGGTGGTCTCGGCGAGGCTTGTGAGAC 468
Qy 379 ACCCGCTTGGCGCGCTTCCACCTTACAGCTGCTTCTTACTGCAAGGGAGCGCTTTCACC 438
Db 469 ACAAGCTTCACTGCTGCTGAGGACACATGCGCATGCGCGTGGAGCG---GCACGCG 525
Qy 439 ATGTGCGCGCGGTGGCGGACGAGCGGCGCACACAGACACCGCGGTCTACGCGCTTCATC 498
Db 526 AGGTGATGCGCGGTGACGCTGACGACACCGCGCTGCGCGCGGTGCTATGCTCATTT 585
Qy 499 GCGCTCTGCTGCTGCTGCGCGCGCTGCTGCGGAGTGGCTCTTCTGCGCTGGAATGTC 558
Db 586 GTGGGCGTGTGGTGGCTCGCGCGCGCTGCGCGCGCTGCTGCGCGCTGCGCGCTGCG 645
Qy 559 CTGTGCGCGCTTTCAGCGCTGCTCCAGCTTTCGCGCGCTTCTACTCCAGCGCTACATCTC 618
Db 646 CTGTGCGCGCTTTCAGCGCTGCTCCAGCTTTCGCGCGCTTCTACTCCAGCGCTACATCTC 705
Qy 619 TTCT-----GCTGTGATCTTTCGCGCGCGCTGCGCGCGCTTCTACTCCAGCGCTACATCTC 666
Db 706 GTGTGCGCGCTTTCAGCGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Qy 667 TATGCGCGCATTTTCGCGCGCTGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 726
Db 766 TTCTTTTACGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 825
Qy 727 GCGCGGAGAGC---GCGCGCGCTGCTGAGAGCGTGTGATGATGATGATGATGATGATG 783
Db 826 TACCGAGAGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885
Qy 784 GTGTGCGCGCGCGCTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
Db 886 GTGTGCTGAGACACGAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939
Qy 844 GCCCAGAGTACCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
Db 940 TCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 999
Qy 904 GTCAACCCCATATCTACTCTTCCGACAGAGGAGTGTGCTGCTGCTGCTGCTGCTG 963
Db 1000 GTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1059
Qy 964 CTGTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1009
Db 1060 CTGTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1105

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RESULT 10  
US-08-861-747-1  
; Sequence 1, Application us/08861747  
; Patent No. 6020158

GENERAL INFORMATION:  
; APPLICANT: MONROE, Donald G.  
; APPLICANT: VYAS, Tejal B.  
; TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
; STREET: 655 15th St., NW, Suite 330 - G Street Lobby  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,747
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jahns, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4610
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1761 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-861-747-1

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Query Match 15.5%; Score 178.8; DB 3; Length 1761;  
Best Local Similarity 53.6%; Pred. No. 1.4e-25;  
Matches 475; Conservative 0; Mismatches 387; Indels 24; Gaps 4;

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Qy 139 GGGGCGCTGCGGGGCTGCTGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 198
Db 187 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
Qy 199 GTGTGCGCGCATTCACGACGACGACGACGACGACGACGACGACGACGACGACGAC 258
Db 247 GTATATGAGCAGCATGCGCTCCACACCGCGCTTCCACACGACCATCTACTGCTGCG 306
Qy 259 AACATCAGCTAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 318
Db 307 AATCTGCGCGCGCTGACCTCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 366
Qy 319 GGGGCGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
Db 367 GGTCCCGGACGACGCGCGCTTTCATCTTACGAGGCTGCTGCTGCTGCTGCTGCTG 426
Qy 379 ACCGCGCTGCGCGCGCTTCCACCTTTCAGCTGCTTTCAGCTGAGGGAGCGCTTTCAC 438
Db 427 ACAAGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
Qy 439 ATGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 498
Db 484 AGTGTGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
Qy 499 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 558
Db 544 GTGGGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 603
Qy 559 CTGTGCGCGCTTTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 618
Db 604 CTGTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
Qy 619 TTCT-----GCTGTGATCTTTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 666
Db 664 GTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
Qy 667 TATGCGCGCATTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
Db 724 TTTTATATGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
Qy 727 GCGCGCAAGCGC---GCGCGCTGCTGAGAGCGTGTGATGCTGCTGCTGCTGCTG 783
Db 784 TACCGAGAGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
Qy 784 GTGTGCGCGCGCATCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843

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APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-948A-3

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Query Match          9.9%; Score 114; DB 2; Length 2185;
Best Local Similarity 51.9%; Pred. No. 2,1e-13;
Matches 416; Conservative 0; Mismatches 360; Indels 26; Gaps 6;

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QY 224 TCGCGTCCGAGCGTGGCTACTATGCTGCTGGTGAACATCAGCTGAGTGAACCTGCTCA 283
DB 1072 TGACGTGTGCGAGTGAGCACTCTCGGCCCAATCTGTCCGGCGCTGACCTCTCTCG 1131
QY 284 CGGGCGGCGCTACCTGGCCCAAGCTGCTGCTGCTGCGGGGCGCGACCTTCGCTGCGC 343
DB 1132 CGGGCGGCGCTACCTCTTCATGATGTTCCACAC-TGTCCCGGACAGCGGCACTTTCAC 1190
QY 344 CCGCCAGTGTCTCTACGAGGAGGCGCTCTTTCACCGCCCTGGCGCGCTTCACACTTCA 403
DB 1191 TTGAGGGCTGTCTCTCGCGAGGGCTTGCTGACACAAACTCTCACTGCTGGTGGCCA 1250
QY 404 GCCTGTCTTCACTGAGGGAGAGCGTTTGCACCATGCTGGCGGCGGCGGAGAGCG 463
DB 1251 CACTGTGTGCGCATGCGCGTGGAGCGGACCGCACTGTGATGCGCTGCACAGCTGCACAGCC 1310
QY 464 GGGCCACCAAGACAGCCGCTCTACGCGCTTCATGCGGCTCTGCTGCTGCTGCGCGCGC 523
DB 1311 GCCTGCGCGCTG---CGCGGTGTGTATGCTCATGTGGGCGTGTGGGTGGCTGCGCTGG 1367
QY 524 TGTGTGGGATGCTGCTTTTGTGGGCTGGAGTGCCTGTGCGCTTTGACCGCTGTCTCA 583

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DB 1368 GCCTGGGCTGCTGCTGCTGCGCCACTCTTGACACTGCTCTGTGCTGCTGACCGCTCTTAC 1427
QY 584 GCCTTCTGCGCCCTTACTTCAATCCAAAGCGTACATCTCTCT-----GCTGTGA 631
DB 1428 GCATGACACCCCTGCTGACACCGCTCTATTTGGCGGTGGCTGTGTGAGACCTGCTTG 1487
QY 632 TCTTCCCGCGCTCTGCGCCACCATCATGAGGCTCTATGAGGSCCATTTCCGCGCTGTGC 691
DB 1488 TCTTCTGCTCATGAGGCTGTGTACACCGCATTTTCTTACGTGTGGCGGCGAGTGC 1547
QY 692 AGGCGAGCGGGAGAGAGGCCCGACCGCCAGCGCCCGCGCAAGGCC---CGCCGCTGC 748
DB 1548 AGCGCATGGCAGAGCATGTCAAGCTGCGACCCCGCTACCGAGAGACAGCTGACGCTGG 1607
QY 749 TGAAGACGTGTGATGATCTGCTGCGCTTCTGTGTGTGTGGGCCCACTCTTGGGC 808
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QY 809 TGTCTGTGGCGGACGCTTTTGGCTCCAACTCTGGGCGCCAGAGATACCTGGCGGCGCATGG 868
DB 1668 TACTGCTCTGTGATGTTTAAAGCTGTGAGTCTGTCA-----ATGTCGTGCGCTTGAANA 1721
QY 869 ACTGATTCCTGCGCCCTGCGCGCTGCTCACTGCGCGGTCAACCCATCATCTACTCTTCC 928
DB 1722 ACTACTTCTACTGTGTGGCGGACCACTCACTGTGATGTGTGTGTGTGTGTGTGTGTGT 1781
QY 929 GCAGCAGAGAGTGTGACAGAGCGGCTGACCTCTCTCTGCTGCGGCTGTCCGCGCTG 987
DB 1782 GAGATGCTGATGATGCGCGGACCTTCCGCGCTTCTCTGCTGTGCGCGCTGCGCGCAG 1841
QY 988 GGCATCGAGAGGCGCGCGGAGCT 1009
DB 1842 TCCACCGCGAGTGTGTCACT 1863

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Search completed: December 13, 2002, 10:15:57
Job time : 86 secs

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